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December 3, 2003, 12:13:45; Search time 897.273 Seconds (without alignments) 1504.579 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AF263366 Mus muscu AC023253 Homo sapi AC005414 Homo sapi AL133230 Human DNA AC135829 Rattus no AL159845 Human DNA AC134046 Cryza sat AC07237 Homo sapi AC073797 Mus muscu AL645625 Mouse DNA AC127560 Mus muscu APO2420 Homo sapi AC002622 Homo sapi AC136859 Rattus no AC128835 Rattus no AC128835 Rattus no AC128835 Rattus no AY086223 Arabidops AS301 Arabidopsis AC011713 Arabidops AC011713 Arabidops AL671893 Mouse DNA AC120853 Mus muscu AC13055 Homo sapi AC010505 Homo sapi AC0060432 Homo sapi AC025513 Homo sapi AC025513 Homo sapi AC061670 Homo sapi AC061670 Homo sapi AC060841 S212P6766 AC124319 Homo sapi AL807252 Mouse DNA AC106568 Rattus no AC133365 Rattus no Homo sapi Rattus no AC108081 Homo sapi AP001492 Homo sapi AC116783 Mus muscu Mus muscu score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AL732445 E AC125640 AC084744 AC127777 AC116186 AC105691 AC137423 AC094294 ALIGNMENTS SUMMARIES AL671893 AC120853 AC128835 AY086223 ATU53501 DB 39443 216261 141832 196055 340000 195718 640 111039 226999 239681 109694 175057 218976 270618 72290 240155 134463 

RESULT 1

	AC108081 . 100808 bp DNA linear PRI 04-MAR-2002			AC108081.2 GI:19073801	HTG.	Homo sapiens (human)		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Sequencing of Human Chromosome 16		
AC108081/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	

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Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
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Submitted (17-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 30-MAY-2000
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                                                                                                                                                                          Submitted (04-MR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CR 94598, USA ON Mar 4, 2002 Uthis sequence version replaced gi:18369927.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                         Direct Submitseion
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Homo sapiens chromosome 18 clone RP11-774P10 map 18q11.2, WORKING
DRAFT SEQUENCE, 37 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 141, 208 genomic DNA of 18q11.2

Published Only in DataBase (2000)

Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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DOE Joint Genome Institute.
Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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* NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7288186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads
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Consensus quality: 117079 bases at least Q40
Consensus quality: 127340 bases at least Q30
Consensus quality: 13354 bases at least Q20
Insert size: 137608; sum-of-contigs
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purces,

Mus musculus (house mouse)

SHTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house)

Selirent, B., Musbaum, C. and Lander, E.

Mus musculus, clone RP24-145D9

L (bases 1 to 168426)

SE Birrent, B., Musbaum, C. and Lander, E.

Mus musculus, clone RP24-145D9

L (bases 1 to 168426)

SE Birrent, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Birrent, B., Linton, L., Nasatien, V., Bloom, T., Boguslavkiy, L., Chosepi, T., Colegelo, W., Calmpas, C., Callymore, A., Cooke, P., Choepel, Y., Colangelo, M., Colline, S., Collymore, C., Parco, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glude, S., Gorte, S., Goyette, M., Marham, L., Grand-Pietre, N., Garders, T., Lehcozky, J., Levine, R., Lindchlad, Toh, K., Liu, G., MacLean, C., Macdorald, P., Major, J., Marquis, N., Matthews, C., Micol, R., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Millenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Millenga, M., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Millenga, M., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Millenga, M., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Mackernan, K., Matches, M., Markernan, K., Matches, M., Millenga, M., Millenga, M., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Millenga, M., Millenga, M., Nachan, R., Markernan, K., Matches, M., Markernan, K., Matches, M., Markernan, K., Matches, M., Markernan, K., Matches, M., Matches, 
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6 140091: contig of 1286 bp in length
2 140191: gap of 100 bp
2 141208: contig of 1017 bp in length.
Location/Qualifiers
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Best Local Similarity 81.24
Matches 26; Conservative
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Wilson, R.K.
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                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1747: contig of 1747 bp in length

* 1848: 103832: contig of 100 bp

* 103833: l03932: contig of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
                                                                                   TITLE
JOURNAL
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JOURNAL
                                                                                                              REFERENCE
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COMMENT

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ROD 04-JUN-2003
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 186768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC127560 186768 bp DNA linear ROD 04-JUN-
Mus musculus chromosome 5 clone RP24-267118, complete sequence.
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933 107966: contig of 4034 bp in length

967 108066: gap of 100 bp

067 119861: contig of 11795 bp in length

862 119961: gap of 100 bp

962 144243: contig of 24282 bp in length

244 14343: gap of 100 bp

344 165641: contig of 21298 bp in length

642 165741: gap of 100 bp

165741: gap of 100 bp

165741: gap of 100 bp

167741: gap of 100 bp

167741: le8426: contig of 2685 bp in length.

167740 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-24 Male Mouse BAC"
1. .1747
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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AC127560.4 GI:31376488
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Best Local Similarity 81.2%;
Matches 26; Conservative
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L Submitted (19-MAY-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1.15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mail:hattori@gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
On Jun 9, 2000 this sequence version replaced gi:8131684.
Center: RIKEN Genome Center Center (GSC)
Center: RIKEN Genomic Sciences Center (GSC)
Center: Attori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Center project Information
Center clone name: RP11-85774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP002420 195637 bp DNA linear HTG 09-JUN-2000 Homo sapiens chromosome 18 clone RP11-857J4 map 18p11.2, WORKING DRAFT SEQUENCE, 61 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Direct Submission
Submitted (04-JUN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63109, USA
On Jun 4, 2003 this sequence version replaced gi:28867181.
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(bases 1 to 195637)

Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Publishes 195,637 genomic DNA of 18p11.2

(bases 1 to 195637)

(bases 1 to 195637)
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NOTE: This is a working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
Consensus quality: 177612 bases at least Q30 Consensus quality: 185076 bases at least Q20 Insert size: 189637; sum-of-contigs Q20 bases; sum-of-contigs Quality coverage: 4.17x in Q20 bases; sum-of-contigs
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NOTE: This is a "working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Direct Submission

Direct Submission

Submitted (06-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA E 4 (bases 1 to 20057)

S DOE Joint Genome Institute.

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Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA S DOE Joint Genome Institute.

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S DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA E 5 (bases 1 to 200557)

S DOE Joint Genome Institute, Stanford Human Genome Center and Los
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Homo sapiens chromosome 16 clone RP11-250E14, complete sequence.
AC009052.8 GI:29124041
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Finishing Completed at Stanford Human Genome Center and Los Alamos
Mational Laboratord.
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.6.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Best Local Similarity 81.2%;
Matches 26; Conservative
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157341:
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Rattus norvegicus clone CH230-482E23, WORKING DRAFT SEQUENCE.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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/mol_type="genomic DNA"
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/chomesee=16"
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50926 a 47625 c 48640 g 53366 t
                                                                                                                                                                                                             Query Match 67.9%; Score 22.4; D
Best Local Similarity 81.2%; Pred. No. 28;
Matches 26; Conservative 0; Mismatches
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 203240: contig of 203240 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Difference Submitted (123-NOV-2002) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON NOV 23, 2002 this sequence version replaced gi:24818546. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scafeold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end in the feature table.
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                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 203240)
Rat Genome Sequencing Consortium.
williams,G., willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Walss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Rat Genome Sequencing Consortium.
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/note="clone_boundary
clone_end:Sp6
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Bandaraniake, D., Barber, M., Barnstead, M., Benahmed, F., Badwin, D., Bandaraniake, D., Barber, M., Barnstead, M., Benahmed, F., Brand, D., Bandar, C., Corkell, T., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cherry, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souaz, L., Davis, C., Derano, C., Penne, C., Evano, C., Hamilton, K., Duval, B., Geer, K., Ganta, R., Garcia, A., Garner, T., Garra, M., Guarrano, C., Hanilton, K., Herrandez, R., Hines, S., Hadun, S.L., Hodgson, A., Hogues, M., Herrandez, R., Hines, S., Hadun, S.L., Hodgson, A., Hogues, M., Marlan, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, J., Liu, M., Liu, Y., Kally, S., Marcia, K., Martin, R., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACL19491 20-NOV-2002 DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-498C19, WORKING DRAFT SEQUENCE, 2 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                      end_sequence:BZ133953"
49878 a 42514 c 41419 g 49473 t 19956 others
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Matches 26; Conservative
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Staturn, Allen, H. Alsbrocks, S. Amin, A. Agquiano, D.
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.
Balden, D., Bandaranake, D., Barbocks, S., Baden, H.
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Mandy, S., Kelly, S., Martin, K., Wartin, 
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Rattus norvegicus clone CH230-98N15, WORKING DRAFT SEQUENCE.
AC128835
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG, HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                     Score 22.4; DB
Pred. No. 27;
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Best Local Similarity 81.29
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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23264889.

The sequence in this assembly is a combination of BAC based reads and whole genome shockun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rab. Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                         Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 239681)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 229827 bases at least Q40
Consensus quality: 232078 bases at least Q30
Consensus quality: 233452 bases at least Q20
Estimated insert size: 237409; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
Center code: BCM This is the site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end_sequence:BH311747"
complement(237496. .238403)
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------- Project Information
Center project name: KAVE
Center clone name: CH230-98N15
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clone_end:T7"
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clone_end:T7
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Unpublished
2 (bases 1 to 239681)
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Unpublished
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                                                                                                                                                                  Best Local Similarity
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                        RESULT 11
ATUS3501
LOCUS
DEFINITION
                                                                    BASE COUNT
ORIGIN
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                           Matches
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This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATC). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or laker ecotypes and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown"
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/brotein_id="AAM67360.1"
/brarein=id=:PREPRCIA340.1"
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GSYVSEMQKSAFQGNILRLIRNEIEYELDHSPPLQPPNSFGPPTVDERPGEQWISLKR
                                                                                                                                                                                                                                                                                                                                                           AY086223 935 bp mRNA linear PLN 14-APR-2003
Arabidopsis thaliana clone 22656 mRNA, complete sequence.
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Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
I bassid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 935)
Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
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Brover.Y., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-Length cDNA from Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 935)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
                                                                                                                                            Gaps
                                                                                             2; Length 239681;
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0
                        4618 others
                                                                                                                                            6; Indels
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                                                                                                                                                                                                                                       32757 GCTCTAGAGCAGCATGGGAGGCAGACAAAGTC 32788
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                                                                                             DB
                                                                                                                                                                                           GCTCTAGACCACCATGGGAAGAAGAGGCGAAGTC 32
                                                                                           Score 22.4; DB
Pred. No. 27;
0; Mismatches
end_sequence:BH311750"
64219 a 53757 c 53551 g 63536 t
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/clone="22656"
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                                                                                                                                                                                                                                                                                                                                                                                                         AY086223.1 GI:21404933
                                                                                             67.9%;
81.2%;
                                                                                           Query Match
Best Local Similarity 81.29
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                       RESULT 10
AY086223/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                      BASE COUNT
ORIGIN
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JOURNAL
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AUTHORS
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JOURNAL
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/map="1; between gl2 and gl7311"
complement(join(834. 963,1063. .1106,1196. .1294,1378. .1490,
1561. .1651,1733. .1819,2062. .2391,2474. .2540,2609. .2667,
2772. .3032,3124. .3189,3271. .3431,4470. .4645,4703. .4881))
/note="theoretical protein with similarity to Swiss-Prot
Accession Number P34881 DNA (cytosine-5-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVSSTEPVESISELEDEEVEENDDIDEASTGAELEPGEFEVEKFLGIMFGDPQGTGEK
TLQLMVRWKGYNSSYDTWEPYSGLGNCKEKLKEYVIDGFKSHLLPLSGTVYTVCGGPP
CQGISGYNYFRNNEAPLEDQKNQQLLVFLDIIDFLKRNYYDLARNVVDLLRFSKGFLAR
HAVASTVANYYQTRLGMAAGSYGLPQLRNYVFLWAAQPSEDLQVGRIQMEFLKLDNA
LTLADAISDLPPVTNYVANDVMDYNDAAPKTEFENFISLRRSETLLPARGGDFTRRLF
DHQPLVLGDDDLERVSYIPKQKGANYRDMPGVLVHNNKAEINDRFRAKLKSGKNVVPA
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VYILCCYAFCFVEMLRGSDASSSLSSDSALNCFENLHKDEKFLLDLYSGCGAMSTGFC
                                                                                                                                                                                                                                                                                             ö
NFGDKEDIKIEATMFDRSVPTSKSTKTEPEYILHITFIVNISKAGATEALEIMCSAWP
DTIEISKLCIRRGINTSPSSYGGPEFEELDDQLQDALYQFLEERGISDELAVFLHRYM
KNKGKAEYVRWMESVKSYVEQK"
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Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-)

Branchyltransferase, zinc finger protein I, nucleoporin 98, poly A+

RNA export protein, plasma membrane ATPase 2, and serine/threonine

protein kinase genes, complete cds.
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/note="similar to PIR Accession Number S55881 zinc finger
protein 1, Arabidopsis thaliana"
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Arabidopsis thaliana
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 37570)
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Submitted (02-APR-1996) John Morris, Molecular Biology,
Massachusetts General Hospital/Harvard Medical School, 50 Blossom
St, Boston, MA 02114, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAISFIKGKSKKPFGRLWGDEIVNTVVTRAEPHNQVSPFAFISHVSGYVPLRIL"
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Goodman,H.M., Gallant,P., Keifer-Higgins,S., Rubenfield,M. and
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A 37.5 Kb sequence from Arabidopsis thaliana chromosome I
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                                                                                                                                                                                                               Length 935;
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/mol_type="genomic DNA"
/strain="Columbia"
                                                                                                                                                                                                                   DB 8;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                   556 crcracaccaradaaaaaaadaraaagr 527
                                                                                                                                                                                                               ch 66.7%; Score 22; DB 1 Similarity 83.3%; Pred. No. 68; 25; Conservative 0; Mismatches
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/chromosome="1"
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                                                                                                               203 g
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CDS

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complement(join(210. 306,392. .573,655. .837,912. .1085,
1163. .1677,1755. .2064,2158. .2262,2340. .3224,3294. .3431,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S., Lee,J.M., Li,J., Gonaziaza, L. Liu,S., Cahano,H., Koo,T., Pham,P., Brooks,M., Howng,B., Chin,C., Choi,B., Chicu,J., Altafi,H., Brooks,S., Chao,Q., Conn,L., Conway,A., Hansen,N., Altafi,H., Johnson-Hopson,C., Khan,S., Kim,C., Lam,B., Nguyen,M., Palm,C., Theologis,A. Tambunga,G., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Arabidopsis thaliana chromosome 1 BAC F23AS sequence
   /protein id="AAA98917.1"
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STOTIKKBSDSVKSYTTKPTVHKIDSVRKGTIPVTBYQLLLGEATNKFSDSNVLSRGR
GCLYACLDBESSVTVKKLTGGGGETDIEKQFENKVIIHKASEDLLDGKELIFPRGSIL
TYMPNRACLDBESSSTVKKLTGGGGETDIEKQFENKVIIHKASEDLLDGKELIFPRGSIL
                                                                                                                                                                                                                                             VPKLSDRANLENILDPAIKGTMDLKHLYQVAAVAVLCVQPEPSYRPLITDVLHSLIPL
LPVELGGSLRIL"
1 7092 c 7104 g 11602 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Submitted (27-07-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 109694)
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Arabidopsis thaliana chromosome 1 BAC F23A5 sequence, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 37570;
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/cul_ivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10189 crcrgcrccaccaradaaaaaaaaaraaar 10218
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 8; Pred. No. 49; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CTCTAGACCACCATGGGAAGAGGGGAAGT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/gene="F23A5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 25; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC011713.2 GI:6136350
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                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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JOURNAL
REFERENCE
AUTHORS
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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LFQYCETWSSMESQRQFIKDLGIPSEWMHEALVRTPYHSSFLLLKVLVAHC"
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24949. 25090,25575. 25355,25408. 25541,25833. 25965)
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Accession Number P41838 poly A+ RNA export protein"
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TTSLSHVFKQSIHQKPTIGKMLPEKFHLEVAGNNNSNNVAAKLERIGHFKSNQEDHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVKHPLMVVGTADRNLIVENLQNPQTEFKRIQSPLKYQTRCVTAFPDQQGFLELACS
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join(27691. .27759,27827. .27964,28035. .28919,28997. .2910
29195. .29504,29582. .30096,30174. .30347,30422. .30604,
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ANWNFARIRGIGWGWAGVIMLYSIVFYIPLDILKFIIRYSLSGRAWDNVIENKTAFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKDYGKGEREAQWAQAQRTLHGLQPAQTSDMFNDKSTYRELSEIADQAKRRAEVARQR
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Accession Number P19456 plasma membrane ATPase 2 (proton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34403. .34644,34725. .32103.33244. .33163,33443. .3369. /note="Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase" /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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CDS

CDS

us-10-082-772-1.rge

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GILBAVGAFTSDDLHTLDMGFVAQLLSQGLCHWAIYVLHIPPREDHPYLHVTVIREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(15961. .16202,16585. .16634,16729. .16781,16917. .17216)
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AQYARRWKIXMDAELGEKKKKEBERKEKERBAEQKALQVBAJTKSHBELMBMRQRLGKI
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SRVISSSYDGLIRLMDVEKSVFDLVYSTDEAIFSLSQRPNDEQSLYFGQDYGVFNVWD
LRAGKSVFHWELHERRINSIDFNPQNPHVMATSSTDGTACLWDLRSMGAKKPKTLSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGNNRVNQDKSCEAENEKKKLTSVSSRERSTIATPSSSSSSPSVQVRGRSRKRPRAL
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WDDSYIYVGNLSKKIDVINPKLKRTVMELHNPLQRAIPCRIHCHPYNVGTLAGSTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Contains similarity to gb|AF151904 CGI-146 protein
from Homo sapiens. EST gb|T44446 comes from this gene."
/codon_start=1
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18946. .19779))
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subunit git5p from Schizosaccharomyces pombe and contains
2 PF|00400WD domain, G-beta repeat domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFQYCETWSSMESQRQFIXDLGIPSEWMHBALVRTPYHSSFLLLLKVLVAHC"
complement (13266. .14507)
/gene="F23A5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oin(20272, .20358,20752, .21074,21168, .21330)
/gene="F23A5.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="F23A5.7"
profect="F23A5.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="AAF14660.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPSSPLTLGSSSV"
15961. .17216
/gene="F23A5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="F23A5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F23A5.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20272. .21330
/gene="F23A5.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene=Fr2as.r.
/gentical to gb|Q38842 RAE-like protein and contains 5 PF|00400 WD domain, G-beta repeat domains.
ESTS gb|T7610, gb|Z37676, g"

Codon_starta.
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/product="F23A5.2(form2)"
/product="F23A5.2(form2)"
/product="F23A5.2(form2)"
/product="F3A5.2(form2)"
/product="F3A6.2(form2)"
/product
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6168. .6309,6444. .6617,6704. .6781,6897. .6983,7470. .7526))
/gene="F23A5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(4792. .4842,4939. .5019,5179. .5250,
329. .5406,5512. .5640,5903. .5983,6168. .6309,6424. .6617,
5704. .6781,6897. .6983,7470. .7526))
/gene="F23A5.2"
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frane="P23A5.3"
/note="identical to gi|1297187 nucleoprotein 98 homolog
from Arabidopsis thaliana cosmid gb|U53501. EST gb|W43800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MATEGAPATANSNPNKSYEVTPSPADSISSLSFSFRADILVATS
WDNOVRCWEISRSGASLASAPKASISHDOPVLCSAWKDDGTTVFSGGCDKQAKMWPLL
SQQPVTVAMHEGPIAAMAN TEGMILLATGSWDKTLKYWDTRQQNPVHTQQLEDKCYT
LSVKHPLMYVGTAADRALIVPRLOVROTFFKZIOSPLKYQTRCVTAFFDQGGFLELACS
LDAYILDGAPNFWDKDSKQRLKVFSSCIDFLFC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKLGDIVPADGRLLDGDPLKIDQSALTGESLPVTKHPGQEVYSGSTCKQGELEAVVIA
TGVHTFFGKAAHLVDSTNQEGHFQKVLTAIGNPCICSIAIGMLIEIVVMYPIQKRAYR
DGIDNLLVLLIGGIPIAMPTVLSVTMAIGSHRLSQQGAITKRWTAIEEWAGNDVLCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTGTLTLNKLTVDKSMVEVFVKDLDKDQLLVNAARÄSRVENQDAIDACIVGMLGDPRE
REGITEVHPFPFPRTAITYIDAGUMHHVSKGAREQITELCHREDASKRAHD
IIDKRADRGIRSLAVORQTVBEKDKNSPGEPMQFIGLIELPPPPRHDSAETIRRALDI
GVNVKMITGDQLAIGKETGRRLGMGTNMYPSSALLGQDKDESIASLPVDELIERADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGV P PEHKYEI VKRLOEMKHI CGMTGDG VNDA PALKRADIGIA VADATDAARSASDIV
LTBPGLSVIVSAVLTSRAI FORMKNYTI YAVSITIRIVMGFMLLALIMKFDFSPFMVL
IVAILNDGTIMTISKDR VKPSPLPDSWKLKBIPATGVVLGTYLAVMTVVFFWAAESTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQLIATLIAVYANWNFARIRGIGWGWAGVIŴLYSIVFYIPLDILKFIIRYSLSGRAWD
NVIENKTAFTSKKDYGKGEREAQWAQAQRTLHGLQPAQTSDMFNDKSTYRELSEIADQ
AKRRAEVARLRERHTLKGHVESVVKQKGLDIEAIQQHYTL"
                                                                                                                                                                                                                                                                                                                                                                                      /tränslation="MagNKDSSWDDIKNBGIDLEKIPIEEVLTQLRCTREGLTSDEGQ
TRLEIFGPNKLEEKKENKVLKFLGFMMNPLSWVMELAAIMAIALANGGGRPPDWQDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFSAKFGVRSISGNPHELTAAVYLQVSIVSQALIFVTRSRSWSYVERPGFWLISAFFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKQRLKAMSRCNQPIPCSSFNHDGSIYAYAACYDWSKGAENHNPATAKSSIFLHLPQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GITVLLIINSTISFIEENNAGNAAALMAGLAPKTKVLRDGKWSEQEAAILVPGDIIS
3499. .3597,3681. .3800,3875. .3931))
/gene="F23A5.1"
/note="Identical to gb|X73676 aha9 (ATAHA9) ATPase gene
from Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Identical to gb|Q38942 RAE-like protein and contains 5 PF|00400 WD domain, G-beta repeat domains. ESTS gb|T76710, gb|Z37676 an"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="F23A5.2(form1)"
/protein_id="AAF14654.1"
/db_xref="G1:6503279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'evidence=not_experimental
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/db_xref="GI:6503280"
                                                                                                                                                                                                                                           /evidence=not_experimental
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/db_xref="G1:6503277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4792. .7526)
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gene

gene

CDS

Query Match

Local

Matches

RESULT 13 AL671893/c LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS

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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 17, clone RP23-343A20
                                                2.
                                                                                                                                                                 128835 GCTCTAGAAACCATGGATAGAATGCGAAG 128806
                                             0; Mismatches
                83.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AC120853.3 GI:28394405
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 218976)
            Best Local Similarity 83.3
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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JOURNAL
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JOURNAL
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JOURNAL
                                                                                                                                                                                                                                                              RESULT 14
AC120853
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             During sequence assembly data is compared from overlapping clones, where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP:, MORMPEP; Information on the WORWPEP database can be found at
/db_xxef="G1;6503284"
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EQWISLKRNFGDKEDIKIEATWFDRSVPTSKSTKTEPEYILHITFIVNISKAGATEAL
EIMCSAWPDTIEISKLCIRRGINTSPSSYGGPEFEELDDQLQDALYQFLEERGISDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL671893 175057 bp DNA linear ROD 02-SEP-2002 Mouse DNA sequence from clone RP23-170G19 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-170G19 is
from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 9, 2002 this sequence version replaced gi:22265401.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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                                                                                                                                                              Length 109694;
                                                                                                                                                                                                                           5; Indels
                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                            21069 CTCTGGTCCACCATAGGAAGAGGGTGAAGT 21040
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37591 c 36564 g 48219 t
                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                  2 CTCTAGACCACCATGGGAAGAAGAGT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                          66.7%; Score 22; 83.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
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1. .175057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                        25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawlor, S.
Direct Submission
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seguence.
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Query Match

BASE COUNT ORIGIN

source

FEATURES

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AC139751 240155 bp DNA linear HTG 21-FEB-2003
Mus musculus chromosome UNK clone RP24-403E24, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 240155)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (12-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 240155)
Mrephrson,J.D. and Waterston,R.H.
Direct Submission
Submitted (21-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases I to 240155)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Mi3; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 236018 bases at least Q40
Consensus quality: 237361 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --------- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACI39751
ACI39751.1 GI:28316668
HTG; HTGS_PHASE1; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.33
Matches 25; Conservative
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Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 15, 2003 this sequence version replaced gi:28173213.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.weahington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                            Center project name: 120496
Center project name: 120496
Center clone name: 343 A 20
Center clone name: 343 A 20
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.966731
Consensus quality: 215262 bases at least Q40
Consensus quality: 217762 bases at least Q30
Consensus quality: 217715 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 217976; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
Quality coverage: 8.1 in Q20 bases; sum-of-contigs
                                                                                                                                                             Center code: WIBR
Web alte: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
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contig of 7493 bp in length
gap of 100 bp
contig of 10890 bp in length
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gap of 100 bp
contig of 1310 bp in length
gap of 100 bp
contig of 4378 bp in length
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f 3599 bp in length
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8 218976: contig of 8319 bp in length.
Location/Qualifiers
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8343. .11941
/note="assembly_fragment"
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vector_side:left"
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/chromosome="17"
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83.3%; Pred. No. 42;
Live 0; Mismatches
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                         se contig of 5576 bp in length
contig of 4481 bp in length
contig of 4481 bp in length
contig of 10577 bp in length
contig of 10577 bp in length
contig of 13323 bp in length
contig of 13323 bp in length
contig of unknown length
contig of unknown length
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contig of 14851 bp in length
contig of 14855 bp in length
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of 29497 bp in length
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of 25521 bp in length
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gap of unknown length
contig of 38818 bp in length.
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note="assembly_name:Contig27"
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note="assembly_name:Contig28"
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ORIGIN
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Search completed: December 3, 2003, 13:18:39 Job time : 904.273 secs

Query Match 66.7%; Score 22; DB 2; Length 240155; Best Local Similarity 83.3%; Pred. No. 41; Matches 25; Conservative 0; Mismatches 5; Indels 0

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Gaps

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us-10-082-772-1.rng

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3, 2003, 12:13:41 ; Search time 157.909 Seconds (without alignments) 564.131 Million cell updates/sec
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| SIDS1/gegdata/geneseq/geneseqn=embl/NA1980.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seg length: 200000000
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33
                                                                                                                                                                                                                             December
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Expression vector	Arabidopsis thalia	Arabidopsis thalia	Lambda integrase P	Plasmid DCXLamintR	Plasmid pCX-Lamint	Artificial plant c	Himmi nemiH
ID	AAF61392	AAC48285	AAC34608	ACC44614	ACC44715	ACC44730	ABT16616	AAK69042
ОВ	22	21	21	25	25	25	25	22
Length	33	933	935	35				
% Query Match	100.0	66.7	66.7	63.6	63.6	63.6	63.6	62.4
Score	33	22	22	21	21	21	21	20.6
Result No.		υ	с С	4	'n	φ	7	œ ن
	% Query Score Match Length DB ID	% Query Score Match Length DB ID 33 100.0 33 22 AAF61392	Score Match Length DB ID  33 100.0 33 22 AAF61392 22 66.7 933 21 AAC48285	Query Score Match Length DB ID 33 100.0 33 22 AAF61392 22 66.7 933 21 AAC4808 22 66.7 935 21 AAC34608	Score Match Length DB ID  33 100.0 33 22 AAF61392 22 66.7 933 21 AAC48285 22 66.7 935 21 AAC34608 21 63.6 35 25 ACC44614	Ouery Score Match Length DB ID 33 100.0 33 22 AAF51392 22 66.7 933 21 AAC48285 22 66.7 935 21 AAC4614 21 63.6 5855 25 ACC44614 21 63.6 5855 25 ACC44614	Ouery Score Match Length DB ID 33 100.0 33 22 AAF61392 22 66.7 933 21 AAC88285 22 66.7 935 21 AAC34608 21 63.6 35 25 ACC44614 21 63.6 5855 25 ACC44730 21 63.6 5855 25 ACC44730	Score Match Length DB ID  33 100.0 33 22 AAF61392 22 66.7 933 21 AAC48285 22 66.7 935 21 AAC44614 21 63.6 5855 25 ACC44614 21 63.6 5855 25 ACC44730 21 63.6 5855 25 ACC44730

encodi	Human CDNA sequenc		ΙΑ. Β.	Modified HIV prote	HΙV	H	H	Oligonucleotide #2	PCR primer #2 used	$\rightarrow$		Human ovarian canc	Human ovarian canc	Lambda integrase E	Artificial plant c	Human brain cell s	Propionibacterium	PCR primer for a N	Shrimp white spot	DNA encoding novel	Human oligonucleot	Human oligonucleot	Human immune/haema	Human immune/haema	Human immune/haema	Human immune/haema	Genomic sequence #	Human immune/haema	Human immune/haema	Shrimp white spot	Human reproductive	Human reproductive	Human cancer relat	Human reproductive	Human digestive sy
AAZ9241	AAH1771		·		·	ABK9153	·	AAA4905		·	ABL77925			ACC4464		AAH57559		AAA15	AAH6273	•	AAH4118		AAK7155	AAK7155	AAK7154	AAK7155	AAS4174	AAK7155	•	•	•		ABN6171	AAL03	AAK89237
244	760	3941 22	650	549	549	549	549							071	071		189			087	244		771	4676	5496		2217	9260	260	5107					
62.4	4.4	62.4	62.4	61.8	61.8	61.8	61.8	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	0.09	59.4	58.8	58.8	58.8	58.8	58.8	58.8	8.8	8.8	œ.	8.8	8.8	8.8	8.83	58.2	58.2	58.2	58.2	58.2
20.6			o.	ö	ö	ö	ö	20	20	20	20	20	20	20	20	o,	19.6	ď	φ.	o,				•	19.4		٠	•	•	٠		•	•		•
6 5	11	12	13	14	15	16	17	G 18	_	20	21	c 55	CA	24	25	c 26	N	28	20	30	31	32	m	m	32 0	m	37	38	ტ ტ	4	4	4	4,	C 44	0 45

## ALIGNMENTS

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect Sequence-specific recombination, SSR, integrase, gene therapy, somatic, targeted integration; Int gene; PCR primer; ss. Expression vector pKEX-2-XR Int gene PCR primer 3343. AAF61392 standard; DNA; 33 BP. 99DE-1041186. 99DE-1041186, 05-JUN-2001 (first entry) WPI; 2001-246016/26. <u>а</u>, (DROE/) DROEGE DE19941186-A1. 30-AUG-1999; 30-AUG-1999; 01-MAR-2001. Synthetic. AAF61392; Droege P; 

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990S-0139455-
990S-0139455-
990S-0139456-
990S-0139459-
990S-0139459-
990S-0139460-
990S-0139462-
990S-0139463-
990S-0139463-
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990S-0139463-
990S-0139463-
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99US-0140991.
99US-0141287.
99US-0142154.
99US-0142055.
99US-0142055.
                                                                             99US-0136392.
99US-0136782.
99US-0137528.
99US-0137502.
99US-013724.
99US-0138540.
99US-0138540.
99US-0138540.
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99US-0140353.
99US-0140354.
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99US-0142920.
99US-0142977.
99US-0143542.
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99US-0144005.
99US-0144085.
99US-0144086.
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99US-0144331.
99US-0144332.
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99US-0144335.
99US-0144352.
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99US-0144884.
99US-0144814.
99US-0145086.
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99US-0139492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145224
99US-0145276
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17 - CUN - 1999)

18 - CUN - 1999)

22 - CUN - 1999)

23 - CUN - 1999)

23 - CUN - 1999)

23 - CUN - 1999)
                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
 ö
                                     This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sometic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                              Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence, ss.
                                                                                                                                                                       Length 33;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 56921.
                                                                                                                                                                   Query Match
100.0%; Score 33; DB 22;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                   Sequence 33 BP; 11 A; 8 C; 10 G; 4 T; 0 other;
                                                                                                                                                                                                            1 GCTCTAGACCACCATGGGAAGAAGAGCGAAGTCA 33
                                                                                                                                                                                                                         1 GCTCTAGACCACCATGGGAAGAAGGCGAAGTCA 33
recombination between att sites
                   Example 1; Page 8; 24pp; German
                                                                                                                                                                                                                                                                                 AAC48285 standard; DNA; 933 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0121825.
99US-0123180.
99US-012348.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0128714.
99US-0128714.
99US-0130449.
99US-0130449.
99US-0130449.
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99US-0132484.
99US-0132485.
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99US-0132487.
99US-0132863.
99US-0134256.
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                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
25-MAR-1999,
01-APR-1999,
06-APR-1999,
16-APR-1999,
19-APR-1999,
21-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
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04-MAY-1999;
05-MAY-1999;
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06-MAY-1999
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Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence; ss.
                                                                                                                  Query Match 66.7%; Score 22; DB 21; Length 933; Best Local Similarity 83.3%; Pred. No. 12; Matches 5; Indels Matches 5; Indels
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana DNA fragment SEQ ID NO: 7243.
                                                                                                                                                                              2 CTCTAGACCACCATGGGAAGAGGCGAAGT 31
                                                                                                                                                                                                                        RESULT 3
AAC34608/c .
ID AAC34608 standard; DNA; 935 BP
  99US-0161405.
99US-0161360.
99US-0161369.
99US-0161361.
99US-0161320.
99US-0161992.
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0121825.
990S-0123180.
99US-0123180.
99US-0125788.
99US-0125788.
99US-012624.
99US-012834.
99US-012834.
99US-012824.
99US-0130891.
99US-0130891.
99US-0130891.
99US-0132484.
99US-0132487.
99US-0132487.
99US-0132487.
99US-0132487.
99US-0132487.
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9908-0134941.
9908-0135124.
9908-0135353.
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                                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana,
 25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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29 MAR - 1999

06 - APR - 1999

08 - APR - 1999

19 - APR - 1999

11 - APR - 1999

21 - APR - 1999

23 - APR - 1999

24 - APR - 1999

30 - APR - 1999

30 - APR - 1999

04 - MAY - 1999

05 - MAY - 1999
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09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                      AAC34608;
    E E E E E E E E E E
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9908 - 0145913

9908 - 0145918

9908 - 0145919

9908 - 0146386

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9908 - 014704

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				PR. 06-00T-1999 PR 07-01999 PR 12-00T-1999 PR 13-00T-1999 PR 13-00T-1999 PR 14-00T-1999 PR 14-00T-1999 PR 14-00T-1999 PR 14-00T-1999 PR 14-00T-1999 PR 14-00T-1999 PR 11-00T-1999 PR 21-00T-1999 PR 21-00T-1999	
		,			
905-0136021. 905-0136392. 905-0136782. 905-0137222. 905-0137502.	9US-0138094. 9US-0138840. 9US-0138119. 9US-0139182. 9US-0139492. 9US-0139454. 9US-0139456.	905-0139459. 905-0139459. 905-0139459. 905-0139460. 905-0139461. 905-0139463. 905-0139463. 905-0139817. 905-0139817. 905-0140353. 905-0140354. 905-0140354.	9US-0141287. 9US-0141842. 9US-0142154. 9US-0142390. 9US-0142390. 9US-0142903. 9US-0142977.	99US-0144005. 99US-0144085. 99US-0144085. 99US-0144331. 99US-0144331. 99US-0144331. 99US-0144334. 99US-0144334. 99US-0144834. 99US-0144884. 99US-0144884. 99US-0144884.	905-0145089 905-0145192 905-0145185 905-0145214 905-0145214 905-0145918 905-0145918 905-0145918 905-0145918 905-0146388 905-0146388
				15-001-1999; 16-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 20-001-1999; 20-001-1999; 21-001-1999; 21-001-1999; 22-001-1999; 22-001-1999; 23-001-1999; 23-001-1999; 24-001-1999; 25-001-1999; 25-001-1999; 25-001-1999; 26-001-1999; 27-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 28-001-1999; 29-001-1999; 29-001-1999; 20	
		22-50-00 R			

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crcrogrccaccaraggaagaggrgagr 527
                                                                                                                                                                                                                 2 CTCTAGACCACCATGGGAAGAAGGCGAAGT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lambda integrase PCR primer SEQ ID NO:3.
                                                                                     / Match 66.7%; Score 22; Local Similarity 83.3%; Pred. No. 1 nes 25; Conservative 0; Mismatch
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC44614 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2003 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200297059-A2.
28-OCT-1999;
29-OCT-1999;
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                                                                                           Query Match
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Matches
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ACC4614
ACC4614
ACC4614
ACC4614
ACC6614
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Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.

05-DEC-2002

30-MAY-2002; 2002WO-US17452

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC

Fleming Leung J, Greene A, Lindenbaum M, Perez C, L. Shellard J; Perkins Stewart

., Ы

WPI; 2003-140461/13.

Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of

Example 4; Page 109; 272pp; English.

The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits sites, where an att site is heterologous to the chromosome chromosome. Also described: (I) a platform artificial chromosome in recombinase catalysed recombination, and (2) a method (MI) for introducing a heterologous nuclaic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nuclaic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachinid, or manmal) by introducing (II) by cell fusion, lipid-mediated transfection microprojectile bombardment or direct DNA transfer into an embryonic coll, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for containing allbrary of ACes comprising random portions of a genome. ACC44012 exemplification of the present invention.

Sequence 35 BP; 11 A; 5 C; 12 G; 7 T; 0 other;

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                         Gaps
                         .
0
       Length
                       .
0
     ore 21; DB 2
red. No. 20;
Mismatches
                                        33
63.6%; bcc.
100.0%; Pre
                                       13 CATGGGAAGAAGCGAAGTCA
                       21; Conservative
    Query Match
Best Local Similarity
                      Matches
                                                      g
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20 CATGGGAAGAGGCGAAGTCA

ö

Gaps

ö

Indels

ŝ

Pred. No. 12; 0; Mismatches

DB 21; Length 935

ACC44715 standard; DNA; 5855

ACC44715;

29-MAY-2003

Plasmid pCXLamIntR nucleotide sequence SEQ ID NO:112.

Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.

Bacteriophage lambda

Synthetic

NO200297059-A2

05-DEC-2002

30-MAY-2002; 2002WO-US17452

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

Ä Fleming Leung J, Greene A, Lindenbaum M, J; Perez C, Shellard Perkins E, Stewart S,

WPI; 2003-140461/13

Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of

Example 4; Page 242-244; 272pp; English.

The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site edirected integration in the presence of chromosome. Also described: (I) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect. reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous or an integral or an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous or an integration or an embryonic cell, preferably a stem cell or an embryonic cell, preferably a stem cell or an embryonic cell, preferably a therapeutic product which is useful for an embryonic cell, preferably a stem cell or an embryonic cell o making a library of ACes comprising random portions of a genome. ACC: to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention. 

Sequence 5855 BP; 1356 A; 1491 C; 1590 G; 1418 T; 0 other;

DB 25; 63.6%; Score 21; Plant artificial chromosome; PAC; transgenic plant; vaccine; blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;

.0-MAY-2002; 2002WO-US17451

WO200296923-A1.

05-DEC-2002.

Unidentified

Artificial plant chromosome related plasmid DNA SEQ ID No 27

1724 CATGGGAAGAAGGCGAAGTCA 1744

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Gaps

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Indels

. 0

ABT16616 standard; DNA; 5855

ABT16616

03-APR-2003

ABT16616;

33

13 CATGGGAAGAAGCCGAAGTCA

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Page

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Chromosome-based platform, artificial chromosome; eukaryotic chromosome, att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a eukaryotic chromosome (I)
                                                                                                                                            Plasmid pCX-LamInt nucleotide sequence SEQ ID NO:127.
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 269~270; 272pp; English.
       Pred. No.
                                                                                                                                                                                                                                                                                                    (CHRO-) CHROMOS MOLECULAR SYSTEMS INC
                                           1724 CATGGGAAGAAGGCGAAGTCA 1744
                                33
100.08; Pre
                                 13 CATGGGAAGAAGGCGAAGTCA
                                                                                          ACC44730 standard; DNA; 5855
                                                                                                                                                                                                                                                          30-MAY-2002; 2002WO-US17452.
                                                                                                                                                                                                                                                                           30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                           (first entry)
                21; Conservative
                                                                                                                                                                                               Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                               WPI; 2003-140461/13.
      Best Local Similarity
                                                                                                                                                                                                                        WOZ00297059-A2.
                                                                                                                           29-MAY-2003
                                                                                                                                                                                                                                          05-DEC-2002
                                                                                                                                                                                                                                                                                                                     Perkins E,
Stewart S,
                                                                                                                                                                                                        Synthetic
                                                                                                           ACC44730;
                                                                                                                                                                                                                                                                                                                                                                                           Interest
                Matches
                                                                        RESULT 6
ACC44730
ID ACC4
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, trNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and chromoses, clockines, growth factors, antibozymes, therapeutic proteins, and resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, of the plant. The nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide sequence represents the DNA of a plasmid used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5855 BP; 1356 A; 1491 C; 1590 G; 1418 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome (YAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.6%; Score 21; DB 2
100.0%; Pred. No. 40;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 256-258; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome (BAC) or a yeast artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 CATGGGAAGAAGCCGAAGTCA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2001; 2001US-294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nethod of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-140436/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHRO-)
chromosome, and permits site-directed integration in the presence of lambda-integrates, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrates. Also described: (1) a platform artificial chromosome in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (1) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform catalificial chromosome, preferably an Aces. (11) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (1) by call fusion, lipid-mediated transfection, by a carrier system, microinjection, microcell fusion, electroporation, call, preferably a stem cell or an embryonic call, preferably a stem cell or an embryonic call, preferably a stem cell or an embryonic call, preferably a stem cell or an embryon (11) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleming E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perez C, Lindenbaum M, Greene A, Leung J, Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5855 BP; 1356 A; 1491 C; 1591 G; 1417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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ive 0; Mismatches
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Gaps

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Query Match Best Local Similarity 100. Matches 21; Conservative

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08-SEB-2000; 2000US-0222080.
08-SEB-2000; 2000US-0222080.
12-SEB-2000; 2000US-0222081.
14-SEB-2000; 2000US-0222397.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0222398.
14-SEB-2000; 2000US-0223365.
14-SEB-2000; 2000US-023363.
14-SEB-2000; 2000US-023363.
14-SEB-2000; 2000US-023363.
14-SEB-2000; 2000US-023363.
14-SEB-2000; 2000US-023363.
14-SEB-2000; 2000US-023363.
15-SEB-2000; 2000US
    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23854
                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
1724 CATGGGAAGAAGCGAAGTCA 1744
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient of genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and canner metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 23854; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 717 BP; 120 A; 197 C; 235 G; 165 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC, Ruben SM;
               17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                  05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483426/52
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. 0 62.4%; Score 20.6; DB 22; Length 717; 85.2%; Pred. No. 45; ive 0; Mismatches 4; Indels 0; CTAGACGACCTGGAAAGAAGGTGAAG 577 4 CTAGACCACCATGGGAAGAAGGCGAAG 30 Local Similarity 85.2 nes 23; Conservative Query Match 603 8 g

Gaps

AAZ92416 standard; cDNA; 2244 BP. AAZ92416; AAZ92416
IID AAZ92416
XXX AAZ
XXX AAZ
XXX DD OF O-0
XXX XXX HUMM
XXX HUMM
XXX HUMM
XXX HUMM
XXX HUMM
XXX AAZ
X

05-JUN-2000 (first entry)

cDNA encoding human deubiquitinating protein Dub12.

Human, deubiquitinating protein, Dubl1; Dubl2; immune disorder, inflammation, allergy; immunosuppressant, antiarthritic, antirheumatoid, antiinflammatory; dermatological; antithyroid; ss.

Homo sapiens

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The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostagiandin transporter (DC-PRT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEA84, HSLJDD7R and RANKE, human MD-1 and human and murine MD-2 proteins Dubl1 and Dub 12, human dendiquitinating proteins Dubl1 and Dub 20, 12, human MD-1 and murine MD-2 proteins. Dubl1 and Dub 20, 12, human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used for modulate uptake of substrates (e.g., prostagianin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proliferation, or differentiation of cells), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, or abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune allergic disorders, or abnormal cellular proliferation, for example, cresponses in which T cell activation, expansion, and/or immuno thyroiditis, systemic lupus erythematosus, Habhimoto's autoimmune thyroiditis, systemic lupus erythematosus, Habhimoto's cell memory play an important role. Sequences AAS22413-232416 represent connected Dubl1 proteins and AAS92415-292416 encode Dubl2 proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                    Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gorman DM;
Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene JR, Johnston JA;
Bazan JF, Mahony D, Lees EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated mammalian genes, used to develop products for treating e.g. immune, inflammatory or allergic abnormalities, cancers or
                                                                       product= "Human Dub12"
note= "No stop codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CTAGACCACCATGGGAAGAAGGCGAAG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 60; Page 192-195; 218pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                              98US-0114466.
98US-0093897.
98US-0132968.
                                                                                                                                                                                                           99WO-US12366
                                                                                                                                                                                                                                              98US-0110938
                                                                                                                                                                                                                                                                                                                       98US-0136214
                                                                                                                                                                                                                                                                                                                                           98US-0099999
                                                     /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative
                                 'partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degenerative conditions
                                                                                                                                                                                                                                                                                                                                                                                 (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-171015/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY77473.
                                                                                                                                  WO200001817-A2.
                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                       2-AUG-1998;
                                                                                                                                                                                                                                                                                                                                             11-SEP-1998;
                                                                                                                                                                   13-JAN-2000.
                                                                                                                                                                                                                                                                                                                       8-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Key
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928 crasacsaccresaaasaasersaas 954

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RESULT 10

RESULT 11

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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length obNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                 sogai T, Nishikawa T, Hayashi K, Saito K, Ya
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 12163; 2537pp + CD ROM; English.
                                                                Human cDNA sequence SEQ ID NO:12163.
          AAH14574 standard; cDNA; 3198 BP.
                                                                                                                                                                                                                                                 Isogai T, Nishikawa T,
                                                                                                                                                                                          11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                         99JP-0248036.
99JP-0300253.
                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                            26-JUN-2001 (first entry)
                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                    Homo sapiens
                                                                                                                   EP1074617-A2
                                                                                                                                                                                  27-AUG-1999;
                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                 Ota T, Is
Ishii S,
                            AAH14574;
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Yamamoto J;

The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonuclectide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence complementary to a
polynucleotide which comprises a 3'-end sequence.
The 5'-end sequence/3'-end sequence is nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesisaling polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18412 represent human cDNA sequences; and AAH13629 to AAH13632
crepresent oligonucleotides, all of which are used in the exemplification
of the processor. of the present invention.

Sequence 3198 BP; 746 A; 1013 C; 881 G; 558 T; 0 other;

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Gaps
                            ;
0
62.4%; Score 20.6; DB 22; Length 3198; 85.2%; Pred. No. 55;
                           Indels
                            4 ;
              Pred. No. 55;
0; Mismatches
              85.2%;
            Best Local Similarity 85.2
Matches 23; Conservative
 Query Match
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1828 CTAGACGACCCTGGAAAGAAGGTGAAG 1854

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4 CTAGACCACCATGGGAAGAGGCGAAG 30

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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonuclectide complementary to the complementary strand of a polymuclectide which comprises one of the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprises a sequence complementary to the complementary strand of a polymuclectide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to the complementary strand of a polymuclectide which comprises a 5'-end sequence and an oligonuclectide comprises a 3'-end sequence complementary to a polymuclectide which comprises a 3'-end sequence of polymuclectide sequence and sequence of complementary to a polymuclectide which comprises at 15 nuclectides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymuclectides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for contains of the full-length cDNAs. The primers are also useful for the full-length cDNAs assily without any specialised methods. AAH13613 to AAH13629 and AAH13631 represent human amino acid sequences; AAB95891 represent human amino acid sequences; and AAH13632 to AAH13632 to feed the contains and an example of the complement of the contains and an example of the complement of the contains and an example of the complement of the contains and an example of the contain
                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length bDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito K,
, Otsuki 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 17312; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.4%; Score 20.6; D
85.2%; Pred. No. 56;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CTAGACCACCATGGGAAGAAGAGGCGAAG 30
                                                                                                                                                                Human cDNA sequence SEQ ID NO:17312
                     BP.
                   AAH17715 standard; cDNA; 3760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                               26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999;
                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001.
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T+
                                                                 AAH17715;
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Mismatches

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Best Local Similarity Matches 23; Conserv

Pred. No.

85.2%;

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셤 ð

AAH17670 standard; cDNA; 4650

RESULT 13 AAH17670

4 CTAGACCACCATGGGAAGAGGCGAAG

Human; primer; detection; diagnosis; antisense therapy; ss.

Human cDNA sequence SEQ ID NO:17234.

Homo sapiens

3P1074617-A2

07-FEB-2001

26-JUN-2001 (first entry)

AAH17670;

28-JUL-2000; 2000EP-0116126

Query Match

DB 22; Length 3941;

Score 20.6;

62.48;

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The present cDNA sequence encodes human ubiquitin protease belonging to the family of mammalian deubiquitinating enzymes. This ubiquitin protease is encoded by the cDNA insert of plasmid deposited with ATCC NO:

PTA-1849. Ubiquitin protease is highly expressed in foetal kidney, testes, foetal liver, ovary and foetal haart. It is also expressed in liver breast, lung, and colon tissue and in liver metastasis derived from malignant colon tissues. Ubiquitin protease is useful for treating disorders mediated by or related to deubiquitinating enzymes, ubiquitin and ubiquitin protease-associated disorders, including neoplasia and tumours of the breast, lung, liver and viral infections. Ubiquitin and ubiquitin protease is useful for treating disorders of liver (hepatic injury, cirrhosis, hepatitis), heart (heart failure, myocardial infarction); kidney (cystic renal dysplasia, glomerulonephritis); breast (periductal mastitis, paget's disease); testis and epididymis (cryptorchidism, crarcphy, inflammations); prostate (nodular hyperplasia); thyroid transmations); prostate (nodular hyperplasia); thyroid carcinoid, obstructive pulmonary disease); colon (idiopathic inflammatory
                                                                                                                                                                                                              Human; ubiquitin protease; cytostatic; virucidal; gene therapy; tumour; neoplasia; hepartic injury; cirrhosis; heparitis; heart failure; rickets; myocardial infarction; skeletal muscle tumour; Grave's disease; atrophy; glomerulonephritis; cryptocrofidism; periductal masticis; Paget's disease; cystic renal dysplasia; polycystic ovarian disease; cretinism; myxoedema; inflammation; obstructive pulmonary disease; osteoprosis; enterocolitis; idiopathic inflammatory bowel disease; bronchial carcinoid; osteomalacia; choriocarcinoma; nodular hyperplasia; metastatic tumour; thyroiditis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skeletal muscle tumours such as rhabdomyosarcoma. Ubiquitin protease DNA is also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     choriocarcinoma); bone disorder (osteoporosis, rickets, osteomalacia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human ubiquitin protease polypeptides, useful for preventing, diagnosing and treating, e.g. breast, lung or liver cancer and viral infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bowel disease, enterocolitis); ovary (polycystic ovarian disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3941 BP; 961 A; 1181 C; 1076 G; 723 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human ubiquitin protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                            AAD03459 standard; cDNA; 3941 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 1; 120pp; English.
                                                                                                                                                                          Human ubiquitin protease cDNA
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                                                                                                                              (first entry)
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/*tag= a
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                                                                                                                              13-JUN-2001
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                                                                                      AAD03459;
RESULT 12
AAD03459
ID AAD03
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligoanclectide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
cligonuclectide comprises at least 15 nucleotides; or (b) a combination
of an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonuclectide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence, where the
cligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence'3'-end sequence is selected from those defined in
the specification. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
particularly full-length cDNAs. The primers are also useful for the
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH31628 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM13633 to AAM18742 represent human cDNA sequences; AAB92446 to AAM13632 abstassent human amino acid sequences; and AAM13629 to AAM13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K, Y.
Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T, Nishikawa T, Hayashi K, Si
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-0300253
1-JAN-2000; 2000JP-0118776
22-MAY-2000; 2000JP-0183767
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Ishii S,
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Modified HIV protein-encoding plasmid DNA #81.

14-AUG-2002 (first entry)

BP.

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ABK91529 standard; DNA; 5549
                                                                           ABK91529;
ABK91529
ABK91529
AC ABK9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                    Gaps
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     Length 4650;
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                                                  Indels
     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                Modified HIV protein-encoding plasmid DNA #80.
Score 20,6; DE Pred. No. 58; 0; Mismatches
                                                                                                                                              Disclosure; Page 562-564; 794pp; English.
                                                                                               4 CTAGACCACCATGGGAAGAGGCGAAG 30
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  62.4%;
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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Best Local Similarity 80.0
Matches 24; Conservative
                                                  Conservative
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Query Match
Best Local Similarity
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                                                  Matches
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ID ABK9
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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Job time : 159.909 secs
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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                                                                                                                                                        Synthetic.
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Gaps

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GCTCTAGACCACCATGGGCGGCAAGTGGAG 1932

1903

RESULT 15

1 GCTCTAGACCACCATGGGAAGAAGGCGAAG 30

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TYPE: DNA ORGANISM: Staphylococcus epidermidis
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Best Local Similarity
Matches 23; Conserv
                        RESULT 2
US-09-134-001C-2470
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17, Appli
18942, Ap
19058, Ap
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370.884 Million cell updates/sec
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                                                                                                                                                        December 3, 2003, 12:13:45 ; Search time 39.2727 Seconds
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    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
!    /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
!    /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
!    /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
!    /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
!    /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-134-0010-2470

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US-08-477-728-110

US-08-477-728-110

US-08-445-51-110

US-08-447-520-110

US-08-446-537-14

US-08-447-728-74

US-08-477-728-74

US-08-477-728-74

US-08-487-20-74

US-08-487-20-74

US-08-487-20-74

US-08-487-20-94

US-08-484-537-74

US-08-484-537-11

US-08-484-537-14

US-08-484-537-94

US-08-484-537-94

US-08-484-537-94

US-08-484-537-94

US-08-484-537-94

US-08-484-537-94

US-08-484-537-94

US-08-38-352-3857

US-08-934-386-7

US-08-934-386-7

US-08-934-386-7

US-08-934-386-7

US-08-934-386-7

US-08-934-386-7

US-08-938-9518-9518
                                                                                                                                                                                                                                                                                                                    1 getetagaceacetgggaagaaggegaagtea 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                           US-10-082-772-1
                        Copyright
                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                     OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                       Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
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22224232109876
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         Sequence 15, Appl
Sequence 16, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 29, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
          US-09-171-025-15
US-09-171-025-16
US-09-171-025-16
US-09-297-751-1
US-09-297-751-1
US-09-313-294A-7202
US-09-313-294A-7202
US-09-313-294A-7202
US-08-45-828A-10
US-08-33-430-10
US-08-33-430-10
US-08-312-283C-360
US-08-312-283C-360
US-08-290-640-24
US-08-290-640-24
US-08-39-214-29
US-08-39-214-29
US-08-39-214-29
US-08-39-214-29
US-08-65-731-1
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kapeller-Libermann, Rosana TITLE OF INVENTION: 23484, A NOVEL HUMAN UBIQUITIN FILE REFERENCE: 5800-51
CURRENT APPLICATION NUMBER: US/09/408,865A
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 3941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1863 cracaccaccricanaacaaccricaac 1889
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                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09408865A Patent No. 6329171 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 62.4%;
1 Similarity 85.2%;
23; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (279)...(3650)
US-09-408-865-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 81.5<sup>3</sup>
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-458-516-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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                                                                                                                                                                                                                                                                                                                                                 Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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COUNTRY: W2

ZIP: 53701-213

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: W1 PC COMPATIBLE FORM: PC-DCS/WS-DOS
SOFTWARE: WAT PC-DCS/WS-DOS
SOFTWARE: WAT PC-DCS/WS-DOS
SOFTWARE: W1 SY 0.00

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 0.3-Dec-1999
CLASSIFICATION NUMBER: 60/110,955
FILING DATE: 0.4-DEC-1998
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 27386
TELEPHONE: G08) 251-5000
TELEPHONE: G08) 251-5000
TELEPHONE: G08) 251-5166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 38584;
                                   Query Match
60.6%; Score 20; DB 4; Length 243;
Best Local Similarity 82.1%; Pred. No. 7.8;
Matches 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                              135 CTCTATAAACAATGGGAAGAAGAGCAAA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Quaries & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                        2 CTCTAGACCACCATGGGAAGAAGGCGAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-453-702B-00
                                                                                                                                                                                                                                                                                                                              APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                     RESULT 3
US-09-453-702B-50/c
; Sequence 50, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1152 Argegaagaagacgaagrea 1133
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// Patent No. 5777085
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 38584
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
US-09-134-001C-2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-458-516-14
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APPLICANT: Co. Man Sung
APPLICANT: To. J. Yun
ITILE OF INVENTION: GIBLILLA
MINNERS OF SEQUENCES:
ADDITION OF SEQUENCES:
ADDITION OF SEQUENCES:
ADDITION OF SEQUENCES:
ADDITION OF SEQUENCES:
CONVEYER REDAINE PORM:
ADDITION OF SEQUENCES:
APPLICATION UNDER: USA
APPLICATION: GOING UNDER
APPLICATION: GOING
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Gaps
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Best Local Similarity 81.5%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, Milliam P.
APPLICANT: COELINGH, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/310,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend Khourie and Crew
                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400;
TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TCTAGACCACCATGGGAAGAAGGCGAA 29
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FILING DATE: 13-FEB-1389
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAMME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear _ MOLECULE TYPE: DNA (oligonucleotide)
MBER: US 07/310,252
13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 110, Application US/08474040
Patent No. 5693761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 114 base pairs
nucleic acid
EDNESS: single
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STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-474-040-110
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Sequence 110.1.
Sequence 110.1.
Set Application US/0847728
GENERAL INFORMATION:
APPLICANT: GUEEN, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED INMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.6%; Score 19; DB 1; Length 114; Best Local Similarity 81.5%; Pred. No. 19; Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ENGRANGE COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                          CURLERY APPLICATION DAIRS

CURASIFICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/210,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY AGENT INFORMATION:
NAME: Smith, William M

REGISTRATION NUMBER: 30,23

REFERENCE/DOCKET NUMBER: 11823-002600

TELEPHONE: (415) 326-2402

TELEPHONE: (415) 326-2402

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEG ID NO: 110:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (oligonucleotide)
US-07-634-278-110
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GENEKAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CAELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
                                                                                                                                  Score 19; DB 1; Length 114;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUDNIKA: US

ZIP: 94301

COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-SEP-1990
APPLICATION NUMBER: US 07/590,975
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 32-DEC-1988
ATTORNEY/AGENT INFORMATION:
ARBIERRATION NUMBER: 11823-002600
TELEPHONE: (415) 326-242
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 3;
Pred. No. 19;
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                             3 TCTAGACCACCATGGGAAGAAGGCGAA 29
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                STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-487-200-110
                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 110, Application US/08484537; Patent No. 6180370; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.6%;
81.5%;
                                                                                                                                  ch 57.6%;
1 Similarity 81.5%;
22; Conservative
TYPE: nucleic acid
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110, Application US/08487200
| Sequence 110, Application US/08487200
| Patent No. 5693762
| GENERAL INFORMATION:
| APPLICANT: CO. Man Sung
| APPLICANT: CO. Man Sung
| APPLICANT: COLINGH, Kailliam P. APPLICANT: COELINGH, Kathleen L. APPLICANT: SELICK, Harold E. TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                   Length 114;
                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EN COMPATIBLE
COMPUTER: EN COMPATIBLE
COMPUTER: IN COMPATIBLE
COMPUTER: IN COMPATIBLE
COMPUTER: IN COMPATIBLE
COMPUTER: IN COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.25
SUSTWARE: PATENTIN RAPE: US/08/487,200
FLING DATE: 7-JUN-1995
CLIASSIPICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-EB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1989
FRIOR APPLICATION NUMBER: 326-2400
FILING DATE: 4110 326-2400
TELEFRANIN (415) 326-2400
TELEFRANIN FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 base pairs
                                                                                                                                                                                                                                                                                                   Query Match
57.6%; Score 19; DB 1;
Best Local Similarity 81.5%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches
  REFERENCE/DOCKET NUMBER: 11823-002600
                                                                                                                                                                                                                                                                                                                                                                                               3 TCTAGACCACCATGGGAAGAGGCGAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                             5 rcracaccaccarccarccarccarccaca 31
                                                                                                            LENGTH: 114 base pairs
TYPE: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-474-040-110
                     TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-487-200-110
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GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 22; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-728-74
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  Gaps
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
  Indels
                                                                                                                                                                                                                                                       APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING APPLICATION 1424
PRICK APPLICATION NUMBER: US 07/590,274
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAMME: SMIGH, WILLIAM M
REGISTRATION NUMBER: 11823-002600
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 Dasse pairs
TWDR: nucleic acid
  5.
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TCTAGACCACCATGGGAAGAAGGCGAA 29
                                          3 TCTAGACCACCATGGGAAGAGGCGAA 29
                                                                                   5 rchadaccaccarddangdarddaga 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (oligonucleotide)
US-07-634-278-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-477-728-74
; Sequence 74, Application US/08477728
                                                                                                                                                                                        Sequence 74, Application US/07634278 Patent No. 5530101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.6%;
Best Local Similarity 81.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i. 132 base pairs
nucleic acid
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
Matches
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ch 57.6%; Score 19; DB 1; Length 132; 1 Similarity 81.5%; Pred. No. 19; 22; Conservative 0; Mismatches 5; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER SEARCH PC compatible
COMPUTER BATCH ISM PC compatible
COMPUTER BATCH ISM PC compatible
COMPUTER ISM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
FRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
FRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-PES-1990
FRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-PES-1999
FRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-PES-1999
FRIOR APPLICATION NUMBER: US 07/290,975
FRIOR APPLICATION NUMBER: US 07/290,975
FRIOR APPLICATION NUMBER: 38-DEC-1989
ATTORNEY AGENT INPORMATION:
NAME: SMITH, WIlliam M
REGISTRATION NUMBER: 30-223
REFERENCE/DOCKET NUMBER: 30-223
REFERENCE/DOCKET NUMBER: 326-2400
TELEDEHOME: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TCTAGACCACCATGGGAAGAGGCGAA 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUEEN, Cary L.
CO. Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COBLINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 74, Application US/08474040 Patent No. 5693761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 132 base pairs TYPE: nucleic acid
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us-10-082-772-1.rni

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GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William F.
APPLICANT: CO. Man Sung
APPLICANT: CANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Razold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.6%; Score 19; DB 1; Length 132; 81.5%; Fred. No. 19;
MEDIUM TYPE: kloppy disk

COMPUTER: BM PC compatible
OPERATURS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSIFICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 18-DEC-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 28-SEP-1990
PRICK APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRICK APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRICK APPLICATION NUMBER: US 07/290,975
FILING DATE: 18-DEC-1988
ATTORNEY/AGENT INPORMATION:
NAME: SMITH, William M
REGISTRATION NUMBER: 30,223
REPERENCE/COCKET NUMBER: 11823-002610
TELEPHONE: (415) 326-2422
INFORMATION FOR SEO ID NO: 74: SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
LYPE: INDICATOR SID 18
TYPE: LINGLER SID 18
TYPE: LINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear _ MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/484,537
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/08484537
Patent No. 6180370
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CTTY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 22, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COBLINGH, Kachleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
TOWNERS OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                  STREET: 3/9 LYLCOL AVELLE
CTTY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEAP Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 13-EB-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/590,975
FILING DATE: 13-EB-1999
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, WILLIAM M
REGISTRATION NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LEBNGTH: 132 DASE DAILS
                             Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTAGACCACCATGGGAAGAAGGCGAA 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (oligonucleotide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/08487200 Patent No. 5693762 GENERAL INFORMATION: APPLICANT: COLEN, Cary L. APPLICANT: CO, Man Sung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 Lytton Avenue
                                                           379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3/2 CITY: Palo Alto
STATE: California
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-487-200-74
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Query Match 57.6%; Score 19; DB 1; Length 134; Best Local Similarity 81.5%; Pred. No. 19; Matches 22; Conservative 0; Mismatches 5; Indels
                                          FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISCRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUTICATION INFORMATION:
TELEPHONE: (415) 326-242
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 base pairs
TYPE: NUCleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December 3, 2003, 14:51:44 Job time: 40.2727 secs
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                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (oligonucleotide)
                      US 07/290,975
                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                              US-07-634-278-94
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Patent No. 5530101
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CO. Man Sung
APPLICANT: COLINGH, Walliam P.
APPLICANT: COLINGH, Wathlen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 3; Length 132;
Pred. No. 19;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
                                                                                     FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/594,279
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENTH: 132 base pairs
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
APPLICATION:
APPLICATION TUBER: US/07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (oligonucleotide)
US-08-484-537-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
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APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.5%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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US-07-634-278-94
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Sequence 11, Applications of the property of t
                                                                                                                                                                                                                   December 3, 2003, 13:18:51; Search time 147.273 Seconds (without alignments) 744.732 Million cell updates/sec
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2. (gn2_6/ptodata/1/pubpna/US07_NEW_PUB.seg:*
3. (gn2_6/ptodata/1/pubpna/US06_NEW_PUB.seg:*
4. (gn2_6/ptodata/1/pubpna/US06_NEW_PUB.seg:*
4. (gn2_6/ptodata/1/pubpna/US08_NEW_PUB.seg:*
5. (gn2_6/ptodata/1/pubpna/US08_NEW_PUB.seg:*
6. (gn2_6/ptodata/1/pubpna/US08_NEW_PUB.seg:*
7. (gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seg:*
8. (gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seg:*
9. (gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seg:*
10. (gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seg:*
11. (gn2_6/ptodata/1/pubpna/US09_NEW_PUB.seg:*
12. (gn2_6/ptodata/1/pubpna/US09_NEW_PUB.seg:*
13. (gn2_6/ptodata/1/pubpna/US09_NEW_PUB.seg:*
14. (gn2_6/ptodata/1/pubpna/US09_NEW_PUB.seg:*
15. (gn2_6/ptodata/1/pubpna/US09_NEW_PUB.seg:*
16. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
17. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
18. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
19. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
11. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
11. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
11. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
11. (gn2_6/ptodata/1/pubpna/US00_NEW_PUB.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-161-403-3
US-10-161-403-112
US-10-161-403-112
US-10-027-632-129494
US-09-918-995-1294994
US-09-918-995-1294994
US-09-918-995-12546
US-09-918-995-12546
US-09-918-995-12546
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US-10-1292-8838-4
US-10-1292-8838-4
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US-10-1292-8838-4
US-10-1292-8838-4
US-10-111-170-50

    getetagaccaccatgggaagaaggcgaagtea 33

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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33
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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RESULT 1
US-10-082-772-1
US-10-082-772-1
Sequence 1, Application US/10082772
Publication No. US20030027337A1
SEQUENCE 1, APPLICATION:
GENERAL INFORMATION:
APPLICANT: DERECH, NICOLE
APPLICANT: LORBACH, ELKE
TITLE OF INVENTION: SEQUENCE-SPECIFIC DNA RECOMBINATION IN BUKARYOTIC CELLS
FILE REFERENCE: DEBE:008US
CURRENT APPLICATION NUMBER: US/10/082,772
CURRENT APPLICATION NUMBER: US/10/082,772
CURRENT APPLICATION NUMBER: DE 199
PRIOR APPLICATION NUMBER: DE 199
PRIOR APPLICATION NUMBER: DE 199
PRIOR APPLICATION NUMBER: DE 199
NUMBER OF SEQ 1D NOS: 20
NUMBER OF SEQ 1D NOS: 20
SOSTWARE PATENT NO NUMBER: DE 199
SOSTWARE PATENT NUMBER: DE 199
SOSTWARE PATENT NO NUMBER: DE 199
SOSTWARE P
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56164, A
56165, A
56166, A
56864, A
56865, A
294164,
294164,
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56165, A
56864, A
56864, A
56865, A
294163,
294164,
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86368, A
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211083,
2738, Ap
2739, Ap
                                             197674,
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  Sequence seq
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
GL-10-082-772-1
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US-10-027-632-197674
US-10-027-632-197675
US-10-027-632-197675
US-10-027-632-197675
US-10-027-632-197675
US-10-027-632-56164
US-10-027-632-56166
US-10-027-632-56166
US-10-027-632-56166
US-10-027-632-56166
US-10-027-632-56166
US-10-027-632-56164
US-10-027-632-56164
US-10-027-632-56164
US-10-027-632-56164
US-10-027-632-56164
US-10-027-632-56165
US-10-027-632-294163
US-10-027-632-211083
US-10-027-632-211083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
    SEQ ID NO 1
LENGTH: 33
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RESULT 2 US-10-161-403-3 ; Sequence 3, Application US/10161403 1724 CATGGGAAGAAGCGGAAGTCA 1744

No. US20030119104A1

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.6%; Score 21; DB 14; Length 35; Best Local Similarity 100.0%; Pred. No. 16; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SLENOTH 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 112, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION. Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Eleming, Elema
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Stewart, Sandra
APPLICANT: Stewart, Ste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Primer: Lamint 1
US-10-161-403-3
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                                                   Perez, Carl
Lindenbaum, Michael
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
Perkins, Edward
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13 CATGGGAAGAAGGCGAAGTCA 33

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SESTING 4

105-10-117 Application US/10161403

Sequence 117 Application US/10161403

Sequence 117 Application US/10161403

Sequence 117 Application US/10161403

APPLICANT: Pertain, Carl
APPLICANT: Sevence 117 Separate 117 Sepa
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APPLICANT Wang, Logeph A.
APPLICANT Wang, Loguan
APPLICANT Wang, Loguan
APPLICANT Wang, Loguan
APPLICANT Slocink, Albert
APPLICANT Greene, Jonathan R.
APPLICANT GREENE GREE
                                                                                                                                                                                            Gaps
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                                                                                                       Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICAMT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastERQ for Windows Version 3.0
SEQ ID NO 12546
LENGTH: 535
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Pred. No. 30;
                                                                                                       DB 11;
                                                                                              62.4%; Score 20.6; D
85.2%; Pred. No. 29;
tive 0; Mismatches
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Best Local Similarity 85.2%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  289 CTAGACGACCCTGGAAAGAAGGTGAAG 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-918-995-12546
| Sequence 12546, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
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Best Local Similarity 85.2%;
Matches 23; Conservative (
                                                                                              Query Match
Best Local Similarity 85.23
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-12546
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; LOCATION: (1)..(2244)
US-09-372-348-14
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                 US-09-918-995-36667
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| Sequence 129494, Application US/10027632
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: 10827.129 |
| TITLE OF INVENTION: 10827.129 |
| TITLE OF INVENTION: 2002-04-30 |
| TITLE OF INING DATE: 2000-07-12 |
| CURRENT FILING DATE: 2000-07-12 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR PILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 1999-11-33 |
| PRIOR FILING DATE: 1999-11-33 |
| PRIOR PILING DATE: 1999-11-33 |
| PRIOR PILING DATE: 1999-10-33 |
| PRIOR APPLICATION NUMBER: US 60/156,358 |
| PRIOR APPLICATION NUMBER: US 60/166,358 |
| PRIOR APPLICATION NUMBER: US 60/146,002 |
| PRIOR APPLI
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Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq. Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REPERBNCE: 2011-756

CURRENT FILING DATE: 2001-07-30

PRIOR PILICATION NUMBER: US/09/235,076

PRIOR PELICATION NUMBER: US/09/235,076

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 GCGCTGGACAACGTGGGAAGCAGGTGAAGTC 308
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                                                                                                                                                                                   Score 20.8; DE
Pred. No. 25;
0; Mismatches
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Best Local Similarity 78.1%; Pred. No. 25;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                   63.0%;
                                                                                                                                                                          Query Match
Best Local Similarity 78.1:
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-027-632-129494/c
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-129494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-10-027-632-129494
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US-09-918-995-36667
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                                                                                               APPLICANT: Addate, Faul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPRENCE: 21012.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 903
LENGTH: 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.6%; Score 20; DB 10; Length 285; 100.0%; Pred. No. 52; 0; Indels ive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 917, Application US/09867701
; Sequence 917, Application US/09867701
; Betent No. US2002013237A1
; GENERAL INFORMATION:
   APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEE
   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
   CURRENT FILING DATE: 2001-05-29
   CURRENT FILING DATE: 2001-05-29
   NUMBER OF SEQ ID NOS: 10912
   SOFTWARE: FASISEQ for Windows Version 4.0
   SEQ ID NO 917
   LENDTH: 331
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Patent No. US20020132237A1
Application US/09867701
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| OTHER INFORMATION: n = A,T,C or G
US-09-867-701-917
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ORGANISM: Homo sapien
FEMTURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-903
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Best Local Similarity
Matches 20; Conserve
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Best Local Similarity
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US-09-867-701-580/c
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                                                                                                                                                                                       Sequence of Application US/10292838

Publication No. US2003015/662A1

GENERAL INFORMATION:
GENERAL FILING DATE:
GENERAL APPLICATION UNDER:
GUNERAL FILING DATE:
GOOG-11-13
FRIOR APPLICATION UNDER:
FILING DATE:
199-11-12
FRIOR FILING DATE:
SOFTWARE:
FRIOR FILING DATE:
SOFTWARE
FILING DATE:
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US-10-292-838-4
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Sequence 12, Application US/10125648

Publication No. US20030077804A1

GENERAL INFORMATION:
APPLICANT: Byrd, Devon R.N.
TATLE OF INVENTION: Compositions and Methods for Recombinational
TITLE OF INVENTION: Compositions and Methods for Recombinational
TITLE REPERENCE: 0942.5240000

TITLE REPERENCE: 0942.5240000

TITLE REPERENCE: 0942.5240000

TITLE REPERENCE: 2002-08-08

PRIOR APPLICATION NUMBER: US 60/284,258

PRIOR PRIOR APPLICATION NUMBER: US 60/284,258

PRIOR PRIOR PRIOR DATE: 2001-04-19

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 12

LENGTH: 55
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60.6%; Score 20; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 12; Length 55; Pred. No. 46;
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                                          928 CTAGACGACCCTGGAAAGAAGAGGTGAAG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 ATGGGAAGAAGGCGAAGTCA 33
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
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US-10-125-648-12/c
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US-09-867-701-903
                                                                                                                                                RESULT 10
US-10-292-838-4/c
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LENGTH: 55
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NAME/KEY: CDS
LOCATION: (1)...(1071)
CTHER INFORMATION: Mucleotide sequence encoding Integrase E147R
US-10-161-403-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.6%; Score 20; DB 14; Length 1071; Best Local Similarity 100.0%; Pred. No. 57; Matches 20; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                           Query Match 60.6%; Score 20; DB 10; Length 340; Best Local Similarity 100.0%; Pred. No. 53; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PETALLA, SCHWALG, APPLICANT: PETALLA, SCHWALG, APPLICANT: Lindenbaum, Michael APPLICANT: Lindenbaum, Michael APPLICANT: Lindenbaum, Michael APPLICANT: Leung, Osephine APPLICANT: Fleming, Elena APPLICANT: Shellard, Joan TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS: FILE REFREENCE: 24601-420 CURRENT APPLICATION NUMBER: 60/294,758 PRIOR APPLICATION NUMBER: 60/294,758 PRIOR PILING DATE: 2001-05-30 PRIOR PILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-05-30 PRIOR FILING DATE: 2001-03-21 NUMBER OF SEQ ID NOS: 129 SOFTWARE: FASUSED for Windows Version 4.0 SEQ ID NO 37 LENGTH: 1071
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SEQ ID NO 580
LENGTH: 340
TYPE: DNA
CREANISM: Homo sapien
US-09-867-701-580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/10161403 Publication No. US20030119104A1 GENERAL INFORMATION: APPLICANT: Perkins, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Integrase E174R
                                                                                                                                                                                                                                                                                                                                                                                           249 ATGGGAAGAAGCGAAGTCA 230
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ORGANISM: Artificial Sequence
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Search completed: December 3, 2003, 17:22:22 Job time: 148.273 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 3, 2003, 12:13:45; Search time 1479.82 Seconds (without alignments) 541.991 Million cell updates/sec OM nucleic - nucleic search, using sw model Title: Perfect score: Run on:

1 gototagaccaccatgggaagaaggcgaagtca 33 US-10-082-772-1 33 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

22781392 segs, 12152238056 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: \* Database :

1: em estba:\*
2: em esthum:\*
3: em esthum:\*
5: em estfor:\*
6: em estgor:\*
7: em estgor:\*
10: gb estg:\*
11: gb estg:\*
12: gb estg:\*
13: gb estg:\*
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15: em estfun:\* em\_estom:\* em\_gss\_vrt:.. em\_gss\_man...... em\_gss\_man...... em\_gss\_mus..... em\_gss\_proi... em\_gss\_proi... gb\_gss\_vri... gb\_gss\_:...

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	* ( 1 5 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	N68492 za14h04.s1	BF540269 602052323	BF301050 602029064	AA622176 nq55g04.s
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æ	Query	Match		21.8 66.1	64.2	64.2	63.6
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400000	6 AU093866 94 AU094204 77 AU165497 195 AU165529 135 PM0-CIO0 144 IL5-CNO0 154 UI-E-ED1	70 UI-H 8 UI-HF 77 QV3- 38 PM0- 01 6027 08 6015 08 6015 15 AGEN	4 0 0 8 0 V N	10 BP23000 132 202479 14 EST2848 10 EST528 11 EST475 11 EST475 110 602750 110 602750
14 CB874 9 AU1823 9 AU1836 9 AL1380 9 AU0934 14 C9857	AU093866 9 AU094204 9 AU165497 9 AU165529 13 BQ32653 10 BF80265 12 BG98264 12 BM72165	12 BQ02727 9 AW503928 10 BW193137 10 BW193137 12 BG76280 10 BB79720 13 BU84903 13 BQ65161	29 CNSO5X52 11 BC02799 11 BC02799 9 AI779832 9 AI482957 9 AI48433	6 9 AW462380 8 10 BB750832 2 9 AW091564 1 12 B1206604 1 12 B1207570 3 9 A1776731 9 10 BG130217 7 12 BG826410 3 10 BF134304 1 10 BF134304
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N N N N N N N N	0 m 4 m 6 r 8 p	O 11 01 10 14 11 10 17 10 01 01 01 01 01 01 01 01 01	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

## ALIGNMENTS

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 462)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kudaba, T., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washurerk EST Project

Unpublished

Contact: Wilson RK

Washington University School of Medicine

4444 Porset Park Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810 N68492 N68492.1 GI:1224653 Homo sapiens (human) ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 N68492 LOCUS DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS

Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Gaps

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/db_xref="taxon:10090"
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Not!; Site_2: Sali; Cloned unidirectionally, Primer: Oligo
dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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401 bp mRNA linear EST 14-OCT-1997
nq55g04.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1147830 3',
mRNA sequence.
AA622176.1 GI:2526052
                                                                                                                                                                                                                                                                                                                                BF301050 957 bp mRNA linear EST 21-NOV-2000 952290641 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4164351 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 977)
IIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conteact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM9449 row: p column: 16

High quality sequence stop: 663.
    Constructed by Life
dT. Average insert size 1.3 kb. Constructed by 1
Technologies. Note: this is a NCI_CGAP Library.
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88.5%; Pred. No. 9.5e+02;
ive 0; Mismatches 3; Indels 0;
                                                                                                   Score 21.2; DB 10; Length 944; Pred. No. 9.5e+02; 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                             GCCCTGGACCACGAGGAGGC 112
                                                                                                                                                                                       1 GCTCTAGACCACGATGGGAAGAAGGC 26
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BF301050
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/not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jefferey B. Green, M.D.
Tissue Procurement: Jefferey B. Green, M.D.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM9520 row: n column: 05
High quality sequence start: 5
High quality sequence stop: 718.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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Seg primer: ml3 -40 forward
High quality sequence stop: 217.
Location/Qualifiers
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Mus musculus
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BF540269 GI:11627650
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BF540269
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Gaps

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us-10-082-772-1.rst

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AU182375
AU182375 Rice panicle at flowering stage Oryza sativa (japonica cultivar-group) cDNA clone E2576, mRNA sequence.
AU182375.1 GI:13896039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryora, viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzea, Oryza.
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tessaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Sasaki, T. and Yamamoto, K.
Rice cDNA from panicle at flowering stage (2001)
Unpublished
                                                                                                                                                                                                                                                                                                                                                       /db_xref="GAB1:561191"
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Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 561 Std Error: 0.00
Plate: 6 row: H column: 21
Seq primer: T7.
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/lab host="DH108"
/cloe="issue rest | Lab host="DH108"
/cloe="issue rest | Lab host="DH108"
/note="organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer: Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
, Triticeae, Hordeum.
1 (bases 1 to 561)
Zhang,H., Weschke,M., Michalek,W., Stein,N. and Graner,A.
EST sequencing and analysis in barley (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                              'PILL'.
CONA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/limage/limage.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 348.
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                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 401)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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HX06H21w HX Hordeum vulgare subsp. vulgare cDNA clone HX06H21
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Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
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                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1147830"
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CB874845
CB874845.1 GI:30076831
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ilarity 82.8%;
Conservative 0
                                    Homo sapiens (human)
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BASE COUNT ORIGIN

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spikaryoza, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzee, Oryza,
I (bases 1 to 569)
Sasaki, T. and Yamamoto, K.
Rice oDNA from panicle at flowering stage (2000)
                                                                                                                                  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKP2); Email s. Wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
No sl sequence available.
This clone (DKP2761P2315) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
1 (bases 1 to 491)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="anygdala"
/dev_stage="adult"
/lab_host="bH108"
/clone_lib="761 (synonym; hamy2)"
/noce="wettor: pSport1; Site_1: Not1; Site_2: Sal1"
136 c 127 g 141 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp761P2315"
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E1031"
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78.1%;
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/clone_lib="Rice panicle at flowering stage"
/note="organ: panicle; Rice cDNA from panicle at flowering
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Spermatophyta, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta, Enthartoideae, Oryza, Magnoliophyta, Liliopsida, Poales, Poaceae,
1 (bases 1 to 460)
Sasaki,T. and Yamamoto,K.
Rice CDNA from panicle at flowering stage (2001)
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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AU183692 Rice panicle at flowering stage Oryza sativa (japonica
cultivar-group) cDNA clone E2159, mRNA sequence.
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
315-8602, Japan
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Pred. No. 1.1e+03;
0; Mismatches 7; Indels
                                                                                               Length 442;
                                                                                          Score 20.8; DB 9;
Pred. No. 1e+03;
0; Mismatches 7;
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DKFZp761P2315_5', mRNA sequence.
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E2159"
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78.1%;
                                                                                          Query Match
Best Local Similarity 78.1%;
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-298-38-7441
Fax: 81-298-38-7468
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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DEFINITION

ACCESSION

BASE COUNT ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

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Query Match Local

Matches

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BASE COUNT ORIGIN

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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DEFINITION

LOCUS

ACCESSION

VERSION

RESULT 10 C98571/c

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
High quality sequence stop: 384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU093866 Auce panicle at flowering stage Oryza sativa (japonica cultivar-group) cDNA clone E0981, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mmny"
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/db_xref="taxon:8355"
/dlone="lnAcB:3405562"
/tissue type="cocytes"
/lab_hogt="DH10B (phage-resistant)"
/clone_lib="NICHD XGC_OOI"
/note="Vector: pGWV-SPORT6; Site_1: Not1; Site_2: Sal1;
/note="vector: pGWV-SPORT6; Site_1: Not1; Site_2: Sal1;
/note="vectorionally. Primer: Oligo dT. Average insert size 2: kb. Constructed by Life Technologies."
a 151 c 151 g 125 t
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; gramatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 604)
Sasaki, T. and Yamamoto, K.
Elice cDNA from panicle at flowering stage (2000)
                                                   Vertebrata; Euteleostomi;
                                                                                               Xenopodinae; Xenopus.
1. (bases 1 to 585)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No. 1.1e+03;
0; Mismatches 7;
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    Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
                                                                                                                                                                                         Tumor Gene Index
Unpublished
Other ESTs: dc82a02.x1
Contact: Robert Strausberg, Ph.D.
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1 Similarity 78.1%;
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
                               Kenopus laevis
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AU093866/c
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/clone lib="Rice panicle at flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering
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/clone_lib="Rice panicle at flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering
stage"
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Oryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryza (oryza (oryza))
1 (bases 1 to 581)
Sasaki,T. and Yamamoto,K.
Eice cDNA from panicle at flowering stage
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Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
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Pred. No. 1.1e+03;
0; Mismatches 7; Indels 0;
                                                                                                                                        Length 569;
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                                                                                                                                                                                           7; Indels
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National Institute of Agrobiological Resources
                                                                                                                                          Score 20.8; DB 9;
Pred. No. 1.1e+03;
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                                                                                                                                          63.0%;
78.1%;
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EST.
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Tel: 81-298-38-7441
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                                                                      124 c
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BASE COUNT ORIGIN

Matches

DEFINITION

RESULT 11

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BF047732

ACCESSION

VERSION KEYWORDS

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Gaps

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/clone="E1731"
/dev stage="flowering stage"
/clone_lib="Rice panicle at flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
I (bases 1 to 658)
Sasaki, T. and Yamamoto, K.
Sice CDNA from panicle at flowering stage (2000)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
I (bases I to 709)
Sasaki, T. and Yamamoto, K.
Rice CDNA from panicle at flowering stage (2000)
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AU165529 GI:11564893
                                                                                                                                                                                                                                                             Contract: Takuji Sasaki
Contract: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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PROJECT ='RGP'.
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba,
305-8602, Japan
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Fax: 81-298-38-7468
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AU165529/c
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/mol type="mRNA"
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                                                                                     /dev stage="flowering stage"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
1 (bases 1 to 657)
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AU094204 Rice panicle at flowering stage Oryza sativa (japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
3105-6602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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Rice cDNA from panicle at flowering stage (2000)
Unpublished
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/mol_type="mRNA"
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Fax: 81-298-38-7468
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SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

AU094204/c LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS

BASE COUNT ORIGIN

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FEATURES

BASE COUNT ORIGIN

RESULT 14 AU165497/c LOCUS DEFINITION

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179 c 137 g 219 t 3 others
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Search completed: December 3, 2003, 14:49:13 Job time: 1483.82 secs

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December 3, 2003, 12:13:45; Search time 1087.6 Seconds (without alignments) 1504.579 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

s Description		60204 Sequence	E36467 DNA polymer	AR044609 Seguence	E05439 Oligonucleo	II3139 Sequence 18	I36498 Sequence 18	X58668 Bacteriopha	M23841 Bacteriopha	L00023 BOP' sequen	AB026619 Nicotiana	10 Hon	Human c	6 Home	176 Mus	X15815 P.polycepha	D8552	AR059	AR063	I9354	M6084	P.falcipar	M91470 Trypanosoma	AY048723 CRIM pla	AX430197 Sequence	AX449167 Sequence	X52304 Chlamydomon	3 6	AR309120 Seguence	N	49 Integrat	150 Integrat	116	733 CRIM	3 Sequence	Mouse pro	m :	Ω, t	AF178452 Integrati	3453	3740	3741	7048715	se(	207455	
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Inclassified.

Inclassified.

AUTHORS

HOSOI,S., Kojima,M. and Kadouchi,S.

TITLE
HIGhly sensitive fluoroassay
JOURNAL

FRATURES

Location/Qualifiers

PAT 17-OCT-2001

ALIGNMENTS

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62.5%; Sura
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E36467.1 GI:13022679
E36467.1 GI:13022679
Bacreriophage lambda
Bacteriophage lambda
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
1 (Dases 1 to 33)
Barnes, U.M.
                                                                                                                                                                                                                                                                                                                                 DNA polymerase having improved heat stability and elevated length and efficiency of primer extension Patent: JP 199239492-A 22 07-SEP-1999;
TAKARA SHUZO CO LID
                                                                               Gaps
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1 (bases 1 to 201)
Okano,K. and Kambara,H.
Polynuclectide capturing support for capturing, eluting and
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/organism='bacteriophage lambda'
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Sequence 18 from patent US 5817506.
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07-SEP-1999
17-DEC-1998 JP 1998359199
19-FEB-1993 US 08/021623
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           /organism="unknown"
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1 (bases 1 to 201)

Okano, K. and Kambara, H.
Separation of polynucleotides using supports having a plurality of electrode-containing cells
Patent: US 5434049-A 18 18-JUL-1995;
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collecting polynucleotides in a sample solution Patent: US 5817506-A 18 06-OCT-1998; Location/Qualifiers
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JP 1993236997-A/11.
synthetic construct
artificial sequences.
1 (bases 1 to 201)
Okano,K. and Kanbara,H.
CHIP FOR CATCHING POLYNUCLEOTIDE
Patent: JP 1993236997-A 11 17-SEP-1993;
HITACHI LTD
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Pred. No. 34;
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100.0%; Pred. No. 3.,
0; Mismatches
                                                                                                                             ore 25; DB 6 red. No. 34; Mismatches
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Sequence 18 from patent US 5434049.
113139.1 GI:910488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OKANO KAZUNOBU, KANBARA HIDEKI
C12Q1/68;
strandedness: Single;
                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial gene
Artificial sequence; Genes.
UP 1993236997-A/11
17-SEP-1993 JP 1992042829
                                                                                                                                                                                                                                                                                                             201 bp
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                                                                                                                                                                                           16 TCATTATTTGATTTCAATTTTGTCC 40
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                                                                                                                                Score 2
Pred.
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Location/Qualifiers
                                                            /organism="unknown"
38 c 27 g
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238. .260
                                                                                    partial"
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Best Local Similarity
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Matches 25; Conserv
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                                                                                                 misc_feature
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LAMINTATT/C
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LAMATTBOP
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Bacteriophage lambda EMBL3 left arm DNA with int gene, partial cds.
X58668.1 GI:15757
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                                                                                                                                                                                                                                         PAT 13-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manninen, I. and Schulman, A.H.
The lambda EMBL3 polylinker and surrounding region for PCR primers
BioTechniques 14 (2), 174 (1993)
93159764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-MAR-1991) A.H. Schulman, Institute of Biotechnology, University of Helsinki P.O. Box 45 (Karvaamokuja 3a), FIN-00014 Helsinki, FINLAND SEE MIN-233, N.A.R. 8:1765-1782(1980) and N.A.R. 16:1633(1988) for overlapping sequences.

See XS8667 for related sequence.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X58668.1 GI:15757
int gene; integrase; polylinker; vector.
Bacteriophage lambda
Bacteriophage lambda
Viruses; deDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                Device for separating polynucleotides having a plurality of electrode-containing cells and movable collecting capillary Patent: US 5607646-A 18 04-MAR-1997; Location/Qualifiers
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                                                                                   Length 201;
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llarity 100.0%; Pred. No. 34;
Conservative 0; Mismatches
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Sequence 18 from patent US 5607646.
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  Location/Qualifiers
                            /organism="unknown"
38 c 27 g
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                                                                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases 1 to 201)
Okano, K. and Kambara, H.
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Best Local Similarity
Matches 25; Conserv
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hes 25, Conserv
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                                                                                                                                                                                                                                                                                                              Unknown
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BOP' sequence from lambda-rifd18, including E.coli insert with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses, debNA viruses, no RNA stage, Caudovirales, Siphoviridae, Lambda-like viruses.

[ Lambda-like viruses.

] [ Lases] [ to 361)

Schmelssner, U., McKenney, K., Rosenberg, M. and Court, D.

Removal of a terminator structure by RNA processing regulates int
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100023 J01640
100023 J01640
100023 J01640
100023 J01640
10162 J1101
ATT site; ATT-lambda site; attachment site; rrnb operon.
Bacteriophage lambda
Bacteriophage lambda
Jruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Location/Qualifiers
Organism="Bacteriophage lambda"
/mol_type="genomic DNA"
/strain="BMBL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.361
/organism="Bacteriophage lambda"
/mol_type="genomic DNA"
/db_xref="taxon:10710"
                                                                                                                                                                                                                                                                                                                DB 7;
34;
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Bacteriophage lambda int gene region.
M23841
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J. Mol. Biol. 176 (1), 39-53 (1984)
84242838
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                                                                                                                                                                         site"
                                                                                                                                                                                                                                  /evidence=experimental
59 c 54 g
                                                                 /db_xref="taxon:10710"
complement(<1...237)
/note="int gene
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Bacteriophage lambda
Bacteriophage lambda
                                                                                                                                                  complement (49. .74)
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                                                                                                                                                complement (49
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Gaps

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us-10-082-772-2.rge

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 717)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.

Not! flanking sequences: a tool for gene discovery and verification of the human genome

Noter Acids Res. 30 (14), 3163-3170 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens genomic sequence surrounding NotI site, clone NB6_767S.
321. .380
/gene="Nspc3"
321. .>380
/gene="Nspc3"
/codon statt=1
/product="phosphoenolpyruvate carboxylase"
/protein.id="Bab83655.1"
/db_xref="G1:20152185"
/translation="MATRNLEKLASIDAQLRALV"
75 c 85 g 115 t
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                                                                                                                                                                                                                          DB 8; Length 380;
34;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="NB6-767S"
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Human dystrobrevin (DIN) gene, e
U84530
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Zabarovsky, E.R.
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HSA332250/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN 22-OCT-2002
                                                                                                                                                                     The attachment site sequences on E.coli (attB) and lambda (attP) contain a 15 bp long complete homology termed common core. Compared with Grantham's data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-APR-1999) Fumihiko Sato, Kyoto University, Departmen of Plant Gene and Totipotency; Kitashirakawa, Sakyo, Kyoto, Kyoto of Selso, Japan (E-mail:fumihikoskais.kyoto-u.ac.jp, URL:http://callus.kais.kyoto-u.ac.jp/callus.html, Tel:81-75-753-6381, Pax:81-75-753-6398)
                                                                                                                                  Original source text: Lambda-rifdl8 transducing phage with E.coli
insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koizumi, N., Toyota, K., Kitajima, S., Yamada, Y. and Sato, F. Genomic structure and promoter analysis of phosphoenolpyruvate carboxylase in a C3 plant, Nicotiana sylvestris Biosci. Biotechnol. Biochem. 66 (8), 1691-1696 (2002) 22246621
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AB026619
AB026619.1 GI:20152184
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                                    Nucleotide sequence of a secondary attachment site for bacteriophage lambda on the Escherichia coli chromosome Nucleic Acids Res. 7 (5), 1335-1341 (1979) 80079294
                                                                                                                                                                                                                                                                                                                                                       /note="common core region secondary att site" complement(203. .368)
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                    Csordas-Toth, E., Boros, I. and Venetianer, P.
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="integration protein (int)"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                 /organism="Bacteriophage lambda"
/mol_type="genomic DNA"
/db_xref="taxon:10710"
115. .129
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Nicotiana sylvestris (wood tobacco)
Nicotiana sylvestris
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/db_xref="G1:215102"
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40 bp upstream from AluI site.
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/transl_table=11
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Sato, F. and Koizumi, N.
Direct Submission
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AB026619
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Length 1090;
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protein_id="AAD27596.2"
db_xref="G1:6532001"
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<291. .>1310
/product="odorant receptor S19"
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                                                         62.5%; scc...
100.0%; Pred. No. Jo.
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/strain="BALB/c"
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                 229 g
/clone="NB1-850S"
265 c 229
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Mus musculus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 1090)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanofhandani,A., Maravenko,O.V.,

Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.

Not! flanking sequences: a tool for gene discovery and verification of the human genome

Nucleic Acids Res. 30 (14), 3163-3170 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSA325746 1090 bp DNA linear PRI 18-JUL-2002
HOMO Sapiens genomic sequence surrounding Notl Site, clone
NB1-8505.
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Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            2 of 23
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 979)
                                                                                                                  Sadoulet-Puccio, H.M., Feener, C.A., Schaid, D.J., Thibodeau, S.N., Michels, V.V. and Kunkel, L.M.
The genomic organization of human dystrobrevin
Neurogenetics 1 (1), 37-42 (1997)
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Sadoulet-Puccio, H.M., Peener, C.A. and Kunkel, L.M.
Direct Submission
Submitted (09-7BN-1997) Genetics, HHMI, 320 Longwood Avenue,
Boston, MA 02115, USA
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ive 0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18912"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AJ325746.1 GI:15870140
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/gene="DTN"
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REFERENCE AUTHORS TITLE JOURNAL

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S (bases 442 to 1421)
S Malnic, B., Hirono, J., Sato, T. and Buck, L.B.
Direct Submission
L Submitted (20-JAN-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
B 3 (bases 1 to 1421)
S Malnic, B., Hirono, J., Sato, T. and Buck, L.B.
Direct Submission
L Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
Sequence update by submitter
Sequence update by submitter
On Dec 7, 1999 this sequence version replaced gi:4680261.
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YRELEDQHVWIAIPFCSMYILALVGNGTILYIITDRALHEPMYLFLCLLSITDLVLC
STYLPRMIAAFURLSHYISYHGCLTQMFFVHAVRATESAVLIAMAFRDRYAICREHY
SITLAMAAFWLGCTARGLLFVPPFVILIERLPFCHHIIPHYCEHMGIAKLACA
SIKRWYNYGKLYACYTRGLLFVPPFVILIERLPFCHHIIPHYCEHMGIAKLACA
SIKRWYNYGKLYALSYTGMDVVLIATSYILLIQAVLRLACHSKOAQFRAFSTGGAHTCH
LVFYIPAFFSFFTHRFGHHVPPQVHIILANLYLLVPPVLNPLVYGINTKQIRLRIF
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Malhio, B., Hirono, J., Sato, T. and Buck, L.B.
Combinatoria! Receptor codes for odors
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AF121976 Innear RC Mus musculus odorant receptor S19 gene, complete cds. AF121976.2 GI:6532000
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/note="G-protein-coupled receptor"
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Sequence of a developmentally transcribed physarum genomic DNA fragment that binds Lupus type-Sm Antibodies

If Inqublished

Inqublished to 1423)

Adams, D.S. and Retter, M.W.

By Adams, D.S. and Retter, M.W.

Direct Submission

In Submitted (13-071-1989) D.S. Adams and M.W. Retter, WORCESTER POLYTECHNIC INSTITUTE, DEPT. OF BIOLOGY BIOTECHNOLOGY, 100

INSTITUTE ROAD, WORCESTER, MA 01609-2280 USA

LOCATION WORLSTER, MA 01609-2280 USA

INSTITUTE ROAD, WORCESTER, MA 01609-2280 USA

ADAMS AND AD
                                                                                                                                                                                                           X15815.
A15815.1 GI:3194
antibody-binding.
Physarum polycephalum (slime mold)
Physarum polycephalum
Bhysarum polycephalum
Bukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physariida;
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                                                   PPGFRA 11-M P.POJYCEPhalum genomic DNA-fragment that binds Lupus type-Sm antibodies.
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62.5%; Score 25; DB 3; Length 1423;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 25; Conservative 0; Mismatches 0; Indels
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promoter

Muthor mast cell produce mast cell produce mast cell produced by the produced produc

Sequencing vector Drosophila melanog Human musculoskele CDNA encoding nove Human musculoskele

cDNA encoding nove Bacillus clausii g Lambda integrase P PCR primer for amp 3382 toxin gene re Reverse PCR primer Reverse PCR primer

B.t. toxin gene PC Bacillus thuringie Probe 618/33F2 for B.t. toxin gene pr Probe #8 used to i

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Sequence-specific recombination of DNA in eukaryotes, useful
particularly for somatic cell gene therapy, uses an integrase to effect
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ACC44615
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ABT16637
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 RESULT
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33F2 reverse prime Bacillus funringie Human prostate exp Bacteriophage lamb Lambca integrase E Arrificial plant c Plasmid pCXLamIntR

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This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sommatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase and formulations comprising it - allowing the amplification of sequences up to 35 kilobases and reducing the mutagenicity generated by the PCR process.
                                                                                                                                                                                                                                                                                                                                                                  AAGGAAAGCGGCCGCTCATTATTTGATTTCAATTTTGTCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermostable DNA polymerase Klenraq-278.

The primers used are Lc5 and Lc3. The template was I de a clone of an R colour control DNA in maize).

(Updated on 25-MAR.2003 to correct PN field.)

(Updated on 25-MAR.2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                    1 AAGGAAAGCGCCCCCCCTTATTTGATTTCAATTTTGTCC
                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 22;
100.0%; Pred. No. 2.7e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The example demonstrates PCR amplification using
                                                                                                                                                                                                                                       Sequence 40 BP; 10 A; 8 C; 8 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33 BP; 7 A; 9 C; 2 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermostable DNA polymerase; PCR primer; ss.
                               Example 1; Page 8; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 52; 79pp; English.
 recombination between att sites
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(first entry)
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9426766-A1
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10-AUG-1995
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AAQ79564
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DB 16; Length 33; 2;

Score 25; Pred. No.

62.5%; 8

Query Match Best Local Similarity

Gaps

Indels 40

Length 40;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Improved polymerase chain reaction method utilizing 2 thermostable DNA polymerases either having or lacking 3'-exonuclease activity and derived from Pyrococcus furiosus, Thermotoga maritime, Thermococcus licoralis and Thermus aquaticus -
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Gaps
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                                                                                                                                                                                           Bacteriophage lambda clone MBL101 specific oligonucleotide.
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 Mismatches
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                         16 TCATTATTTGATTTCAATTTTGTCC
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95US-0483535.
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                                                                                                                 AAD42556 standard; DNA; 33
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ses 25; Conservative
 25; Conservative
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07-JUN-1995;
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AAD42556
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Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
                                                                                                                                                                                                                                                                                          The sequences given in AAQ50309-26 are probes which were used on a chip for capturing a number of target polynucleotides. A group of these probes may be attached on cells which form part of a single chip. The oligonucleotides to be detected are labelled and are complementary to the set of capture probes used. The detection chip may be used to detect a number of different polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleming E;
                                                                                                                                                                                                               Chip for capturing polynucleotide - has several different complementary probes fixed on cells at different sites on single
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Probe; chip; cell; detection; label; capture probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greene A,
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Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                 Disclosure; Page 8; 10pp; Japanese
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21-MAR-2002; 2002US-366891P.
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Les 25, Conservative
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                                                                                                                                                           (HITA ) HITACHI LID
                                                                                                                                                                                     WPI; 1993-330600/42
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Stewart S,
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising readom portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention.
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blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                 Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other;
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                                                                                                             Example 2; Page 207; 272pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABT16636 standard; DNA; 282 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-140436/13.
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ABT16636
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Producing artificial chromosome by introducing a nucleic acid into

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regions with e
nucleic acids
                                                                                                                            WO9940225-A1.
                                                                                                                                      05-FEB-1999;
                                                                                                                                          09-FEB-1998;
12-FEB-1998;
                                                                                                                                                        Worley PF,
Nikolich K,
                                                                                                                                 12-AUG-1999
                                                                                                                        Rattus sp.
                                                                                              AAZ30709;
                                                                Query Match
                                                                                     RESULT 7
AAZ30709/c
                                                                     Matches
                                                                                          à
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.1345 /\*tag= \*tag= \*tag= Rat cryptdin 2 gene. WO9616075-A1 05-OCT-1995; 10-MAY-1996 Rattus sp. AAT30737; intron Key noxe AAT3073 8 The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods insertion of heterologous DNA into plant artificial chromosome (PAC) is useful for producing a transgenic plant chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, FNRA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This producing plant artificial chromosomes of the invention. plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic Immediate early gene; IEG; neuron; brain; function; growth factor; transcription factor; signal transduction; cytoskeletal protein; metabolic enzyme; learning; memory; synaptic transmission; tolerance; neuronal plasticity; ds. Gaps Scheek ; 62.5%; Score 25; DB 25; Length 282; 100.0%; Pred. No. 2.7; 0; Indels Kuner R, Rat neuronal immediate early gene cDNA clone R280. Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other; Hiemisch H, 100.0%; Pred. .... (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. (BADI ) BASF-LYNX BIOSCIENCE AG: Disclosure, Page 263-264; 269pp; English. 243 TCATTATTTGATTTCAATTTTGTCC 267 16 TCATTATTTGATTTCAATTTTGTCC 40 Goetz B, AAZ30709 standard; cDNA; 1763 BP 99WO-US02462. 98US-0074135. 98US-0074518. 05-JAN-2000 (first entry) 25; Conservative Lanahan A, , Zhukovski! WPI; 1999-590697/50. Local Similarity

Novel genes and polypeptides, useful for treating conditions related to a deficiency in nIEG responsiveness to a stimulus

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This sequence represents rat neuronal immediate early gene (IEG) cDNA clone R280. An IEG is a gene whose expression is rapidly clonemediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode a variety of proteins, con neuronal IEGs have been found to encode a variety of proteins, including transcription factors, cytoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in, for example, learning, memory, synaptic transmission, tolerance and neuronal plasticity. Neuronal IEGs neuronal IEG protein products, calls expressing neuronal IEGs and antibodies against neuronal IEG creteins can be used to treat an animal with a deficiency in neuronal IEG can be used to treat an animal with a deficiency in neuronal IEG can be used to treat an animal with a stimulus comprises a maximal electroconvulsive selfcers may be a reduced or elevated level of expression of an IEG. The neuronal stimulus comprises a maximal electroconvulsive selfaure and its effects influence learning or memory. The IEGs and protein products are useful in identifying compounds that modulate the expression or activity of IEG nucleic acids or proteins, respectively.
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/note="exon 1 codes for the 5' untranslated
region and cryptdin-1 prepro sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 25; DB 20; Length 1763; 100.0%; Pred. No. 3.5; 0; Indels 0; Indels 0
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(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 TCATTATTTGATTTCAATTTTGTCC 179
laim 1; Page 114-115; 134pp; English.
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Best Local Similarity 100.
Matches 25, Conservative
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fructosyl transferase; levan sucrase; nitrogen transporter protein;
pathogen resistance; plant; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tissue-specific promoters from Beta vulgaris, useful e.g. for altering carbohydrate metabolism, express transgenes selectively in
                                                                                                                                                     The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity against a broad range of intestinal and opportunistic pathogens. Rat cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2 gene, or corresponding cDNA (see also T30734), can be used to produce large amounts of cryptdin-2 for use in treating inflammatory pathologies of the intestine.
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                                                                                                                                                                                                                                                                                                              Score 25; DB 17; Length 2408;
Pred. No. 3.6;
                                                                          New isolated cryptdin peptide(s) - which have antimicrobial activity, used partic. in the detection and treatment of inflammatory pathologies
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                      Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                      62.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                             Claim 31; Page 64-65; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN81284 standard; DNA; 3049 BP
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2928..3049
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2877..2883
/*tag= c
                                    WPI; 1996-268527/27.
P-PSDB; AAR98787, AAR98792
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                                                                                                                                                                                                                                                                                                                                          25; Conservative
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity
             Ouellette AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1207204-A1
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                                                                   The invention relates to a promoter (A) that is: (i) any of the sequences ABN81281-ABN81284; (ii) the complement of (i); or (iii) a sequence that hybridises to (ii). (A) are used, specifically in Beta vulgaris, to control expression of transgenes, particularly to alter carbohydrate metabolism; reduce loss of storage substances; express invertase inhibitor, fructosyl transferase, levan sucrase or genes that encode transporter proteins for nitrogen compounds, or increase resistance to, or tolerance of, pathogens. (A) provide tissue-specific transgene expression, either in roots or above-ground parts, so avoid pleiotropic effects, e.g. when expressing invertase inhibitor.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA fragment obtainable from Arabidopsis thaliana is capable of promoting root knot and cyst nematode-inducible transcription of an associated DNA sequence when reintroduced into a plant. The promoterless GUS construct binary vector pMOGS53 was mobilised by triparental mating to Agrobacterium tumefaciens MOGIO1 and the resulting strain was used for Arabidopsis root transformation. Line pMOGS53#25 was identified as a line which showed strong GUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter; nematode feeding site; root knot nematode; cyst nematc
Meloidogyne incognita; Heterodera schachtii; Globodera pallida;
transgenic plant; pest resistance; crop protection; ds.
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                                                                                                                                                                                                                                                                                                    62.5%; Score 25; DB 24; Length 3049; 100.0%; Pred, No. 3.7; ive 0; Mismatches 0; Indels (
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plant reduced susceptibility to plant parasitic nematodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis nematode feeding site-preferential promoter.
                                                                                                                                                                                                                                                                   Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 other;
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/codon_start= 3482..3484
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                                    Claim 1; Page 30-31; 57pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana ecotype C24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV34987 standard; DNA; 3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-EP06472
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                                                                                                                                                                                                                                                                                                                                          25; Conservative
roots or aerial parts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOGE-) MOGEN INT NV.
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                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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ID AAV3
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expression inside syncytia and giant cells induced by the cyst nematode Heterodera schachtii and the root knot nematode Meloidogyne incognita, respectively. Promoter tags from line pMGS53#25 were sequenced. The claimed DNA fragment is nematode feeding of stee-specific. Also claimed DNA fragment is nematode feeding of above sequence capable of promoting root knot and cyst nematode inducible transcription of an associated DNA sequence comprising a DNA fragment as above plus a DNA sequence which is not naturally under its transcriptional control, and which causes the production of a plant cell-disruptive substance, preferably barnase; (3) a plant cell-disruptive substance, preferably barnase; (4) a replicon comprising the chimeric DNA sequence of (2), or the above DNA and at least I restriction endonuclease recognition site; (4) a microorganism containing the replicon of (3); (5) a plant cell and consisting of the cells of (5), preferably a dicotyledonous plant, ceppecially a potato plant; (8) a plant grafted onto the root system of a plant of a plant, selected from seeds, flowers, tubers, consisting of the cells of (5), preferably a dicotyledonous plant, (6) a part of a plant, selected from seeds, flowers, tubers, crocts, leaves, fruits, pollen and wood, obtained from the plant of the DNA fragment can be used to identify subfragments capable of crocts, leaves, fruits, pollen and wood, obtained from the plant.

CT or (8), and (10) a crop consisting of the plants capable of crocts, leaves, fruits, pollen and wood, obtained from the plant.

CT can also be used for making hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be used for transforming claimed and the cells of consisting the plants of capacities and be used for transforming consisting can be used to reduce the cells of capacities of capacities and be used for transforming capable of capacities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.5%; Score 25; DB 19; Length 3484; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 25; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       susceptibility of a plant to parasitic nematodes.
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/note= "contains introns"
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/number= 2
2298..2563
/*tag= f
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2012..2177
/*tag= d
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1873..2011
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
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Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma; tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria; antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This nucleotide sequence includes a coding region for mouse mast cell protease 6 (mMCP-6, see AAW64242). The invention provides: compositions comprising an isolated tryptase-7 (such as mMCP-7, see AAW64231), a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product; a nucleic acid encoding a serine protease (SP); and a method of producing a mature SP. Tryptase-7 polypeptides can be used for treating disorders mediated by undesirable thrombus clot formation and amyocardial infarction and recorlusion following thromboembolism, deep vein thrombosis, cerebral embolism, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compositions containing tryptase-7, e.g. mouse mast cell protease-7 - are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.5%; Score 25; DB 19; Length 3757; Best Local Similarity 100.0%; Pred. No. 3.8; Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse mast cell protease (mMCP-6) nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vein and peripheral arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 68-69; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 icarrarrigarricaarrigic 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TCATTATTTGATTTCAATTTTGTCC 40
                                                                                                                                                                                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV42708 standard; cDNA; 3757
                                                                                                                                                                                                                                                                               97WO-US21620.
                                                                                                                                                                                                                                                                                                            96US-0032354.
                                                                                                                      /*tag= i
/number= 4
2934..3098
/*tag= j
              2564..2696
/*tag= g
/number= 3
                                                             697..2860
                                                                         /*tag= h
/number= 4
                                                                                                        861..2933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-1998 (first entry)
                                                                                                                                                                                       number=
number=
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-333308/29.
                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW64242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thromboembolism
                                                                                                                                                                                                                                                                              25-NOV-1997;
                                                                                                                                                                                                                                                                                                            04-DEC-1996;
                                                                                                                                                                                                                  WO9824886-A1
                                                                                                                                                                                                                                                 11-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                         Stevens RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV42708;
                intron
                                                                                                        intron
                                                                                                                                                        exon
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                                                             exon
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ID AAV4
XX AAV4
XX AAV4
XX AAV6
XX XX MABE
KW MABE
KW TYJE
KW AARE:
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4
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one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACes) (1) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (1) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid molecule fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous making a library of ACes comprising random portions of a genome. ACC44612 exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                           comprising
                                                                                   Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
     Fleming E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial plant chromosome related plasmid DNA SEQ ID No 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 25; Length 4346;
                                                                                                                                                                                                       The present invention describes a eukaryotic chromosome (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other;
      Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
      Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
62.5%; Score 25; DB 25
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                      Example 3; Page 244-245; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4298 TCATTATTTGATTTCAATTTTGTCC 4322
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(AGRI-) AGRISOMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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     Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 TCATTATTTGATTTCAATTTTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT16615 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2002; 2002WO-US17451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2001; 2001US-294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fabijanski SF,
     Perez C, L:
Shellard J;
                                                    WPI; 2003-140461/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200296923-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-2002.
   Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABT16615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perez C,
                                                                                                                                     interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant
blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                    This represents the cDNA sequence of the mouse mast cell protease (mMCD-6). The invention provides sequences shown in AAW63160 to AAW63169 that are inhibitors of mMCP-6. These peptides which are tryptasse-6 complex inhibitors, can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, urticaria and anticedema, eczematous dermatitis (atopic dermatitis), hyperproliferative skin disease, anaphylaxis, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory skin conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
hyperproliferative skin disease, peptic ulcer, hyperresponsiveness, inflammatory skin condition, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 3757;
3.8;
                                                                                                                                                                                                                                                                                                                      Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 62.5%; Score 25; DB Similarity 100.0%; Pred. No. 3.8 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 rcarratricarricaarrirgic 485
                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Pages 42-43; 69pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATTATTTGATTTCAATTTTGTCC 40
                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC44716 standard; DNA; 4346 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                                                                                    97US-0037090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2002; 2002WO-US17452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2003 (first entry)
                                                                                                                                                                                                                                                    Huang C, Stevens RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda
                                                                                                                                                                                                                                                                                     WPI; 1998-437390/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200297059-A2
                                                                                                                                                                                    05-FEB-1997;
                                                                                                                                                30-JAN-1998;
                                                                                 WO9833812-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-2002
                                                                                                                  06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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Gaps

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Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with aquivalent amounts of euchromatic and heterochromatic nucleic acids
                                                        Example 19; Page 255-256; 269pp; English.
      WPI; 2003-140436/13.
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial drivomosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, FNRA, rbNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, and proteins, antigens, hormones, cytokines, growth factors, antigens, hormones, cytokines, growth factors, antigens, hormones, cytokines, growth factors, antigens, nature and plant artificial nutrient use and/or improves the nutrient quality of the plant. The nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid growth in a bacterial artificial cherented and or improves the nutrient quality of the plant. The heterologous nucleic acid growth a bacterial artificial chromosome (YAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents the DNA of a plasmid used in the Score 25; DB 25; Length 4346; Pred. No. 3.9; Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other; chromosome (BAC) or a yeast artificial method of the invention

0; Indels Mismatches 40 16 TCATTATTTGATTTCAATTTTGTCC 0; 62.5%; 8 Conservative Query Match Best Local Similarity Local 25; Conserva

4298 rcarrarirdarircaarirrercc 4322

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Gaps

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AAT18924 standard; DNA; 4909 BP AAT18924; AAT18924/c RESULT 15 

(first entry) 17-JAN-1997

Plasmid pA126i

Spider; dragline protein; variant; monomer; polymer; circular; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating; ss. Spider;

Synthetic

WO9429450-A2

22-DEC-1994,

15-JUN-1994;

93US-0077600. 15-JUN-1993;

94WO-US06689

(DUPO ) DU PONT DE NEMOURS & CO

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Fahnestock SR;

WPI; 1995-036479/05.

New synthetic variants of spider dragline protein - for making

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This sequence represents the complete nucleotide sequence of the plasmid was used in the construction of the vector pFP510 which was used to express synthetic spider dragiline variants, DP-1A.9 and DP-1B.9 pAJ26i comprises a replication origin active in E. coli, a selectable genetic marker which is a gene conferring resistance to a melectable genetic marker which is a gene conferring resistance to consistent in sites for the restriction endouncleases Bamil and BglII with no essential sequences between them, and a third restriction site for peri, located within the selectable marker which produces cohesive ends incompatible with those produced by Bamil and BglII. The polypeptide incompatible with those produced by Bamil and BglII. The polypeptide mornmers are variants based on a consensus sequence derived from the fibre forming regions of goider dragiline protein, esp. the natural protein and the pattern of variation among individual repeats. Of the natural protein and the pattern of variation among individual repeats. DP-1A analogues are composed of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus componer which comprises four repeats which differ from the consensus (1) the polyvalanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence; is deleted, consensus integral multiples of three consecutive residues; (3) aside from the polyvalanine sequence, deletions usually encompass integral multiples of three consecutive residues; (1) the polymalanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The proteins may be used to produce fibres of high tensile strength elasticity, suitable for clothing, rope, surgical sutures, biomateri for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (5) a repeat in which the entire poly-alanine sequence is deleted is generally preceded by a repeat containing six alanine
fibres useful as clothing, surgical silk, plastic reinforcement
etc., also related DNA, vectors and transformed cells
                                                                                         English.
                                                                                      Example 1; Fig 13; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the same sequence; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues.
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ö 62.5%; Score 25; DB 16; Length 4909; 100.0%; Pred. No. 4; Indels . 0 100.0%; Pred. No. 16 TCATTATTTGATTTCAATTTTGTCC 40 25, Conservative Local Similarity Query Match Best Loca Matches ଚ

Seguence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 other;

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Gaps

3, 2003, 12:23:35 December Search completed: Decemi Job time: 192.405 secs

2288 icainairicairicaairirgic 2264

a

Sequence

App1:

Sequence Sequence Sequence

Sequence 2 Sequence 2

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Sequence 26,
Sequence 26,
Sequence 26,
Sequence 26,
                                                                               Sequence
               Sequence
Sequence
Sequence
                                                      Sequence
                                                                                                                                                                                                                                                                                       . HOSOI, Shigeru

KAOIMA, Makiko

KADOIKHI, Sachiko

TITLE OF INVENTION: HIGH SENSITIVITY FLUOROIMMUNOASSAY

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: PILLSBURY, MADISON & SUTRO

STREET: 1100 NEW YORK AVENUE, N.W.

STATE: D.C.

COUNTRY: USA

ZIP: 20005

WPUTER RFPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: FC-DOCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,223C
FILING DATE: 09-Feb-1998
CLASSIFICATION: <UNINCOMNATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul E. White, Jr.
REGISTRATION NUMBER: 32,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
US-09-107-532A-31
US-09-453-702B-66
US-09-453-702B-66
US-08-485-568A-3
US-08-357-698-5
US-08-357-698-5
US-09-357-206A-3
US-09-357-206A-9
US-09-357-306A-9
US-09-357-364-368-36
US-09-124-698-26
US-09-124-698-26
US-09-124-698-26
US-09-124-523-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.5%; Score 25; DB 3; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEK: 6714627CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic acid
STRANDEDNESS: Single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 TCATTAITTGATTTCAATTTTGTCC 40
                                                                                                                                                                                                                                                                                                                      ; Sequence 5, Application US/09011223C; Parent No. 6255048; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPOLOGY: Linear
               9827
1132
3561
3561
3561
3561
3561
4281
10881
12286
2377
2377
                                                                                                                                                                                                                                                                                                             US-09-011-223C-5
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                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    December 3, 2003, 12:13:45; Search time 47.6033 Seconds (without alignments) 370.884 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, A Sequence 18, Sequence 18, Sequence 18, Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69,
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Sequence
Sequence
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Sequence
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                                                                                                                                                               1 aaggaaagcggccgctcattatttgatttcaattttgtcc 40
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'cgn2_6/ptodata/1/ina/5A_COMB.seq:*
'cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6A_COMB.seq:*
'cgn2_6/ptodata/1/ina/6B_COMB.seq:*
'cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-011-223C-5
US-08-0410-544-18
US-08-1728-7854-18
US-08-18-728-7854-18
US-08-18-728-69
US-08-18-278-69
US-08-18-278-69
US-09-18-278-69
US-09-340-090-1
US-09-310-090-1
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                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                     US-10-082-772-2
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24408
34408
3484
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3757
534909
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Perfect score:
                                                                                                                                                                                          Scoring table:
                                                           OM nucleic
                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                    Run on:
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No.
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Gaps

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COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NAPA:
RILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NAMBER: 08/410,544
FILING DATE: 21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 rcarrarraarraaarrirarca 154
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TELEFAX: 202-0...
TELEFAX: 202-0...
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                 COUNTRY: US
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-410-544-18
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                                                                                                                           Sequence 18, Application US/08021667A
Patent No. 5444049
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kanbara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
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CONTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
CLASSIPICATION: 435
ATCHASTING: 435
ATCHASTATION: A35
ATCHASTATION: WHERE: 20.178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELEPHONE: 202-828-0300
TELEFHONE: 202-828-0300
TELEFAX: 202-828-0300
TELEF
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Suite 600, 1919 Pensylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 25; DB 100.0%; Pred. No. 0.3 iive 0; Mismatches
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2 TCATTATTTGATTTCAATTTTGTCC 26
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US-08-410-544-18
; Sequence 18, Application US/08410544
; Patent No. 5607646
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli,
STREET: Suite 600, 191
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.5
Best Local Similarity 100.
Matches 25; Conservative
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US-08-021-667A-18
                                                                                    RESULT 2
US-08-021-667A-18
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Length 201;
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COMPUTER ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: DEM PC Compatible
COMPUTER: DEM PC Compatible
COMPUTER: DEM PC Compatible
COMPUTER: DEM PC COMPUTER:
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/410,544
FILING DATE: US/08/410,544
FILING PAPLICATION NUMBER: US/08/410,544
FILING DATE: 24-FEB-1993
ATPORNEY/AGBAT INPORMATION:
NAME: TELECOMMUNICATION NUMBER: SO.178
REGISTRATION NUMBER: SO.178
REGISTRATION NUMBER: SO.178
REFERENCE/DOCKET NUMBER: SO.178
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-828-0380
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100.0%; Pred. No. 0.38;
tive 0; Mismatches
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Gaps
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Sequence 69, Application US/08482279
Sequence 69, Application US/08482279
Sequence 69, Application US/08482279
Sequence 69, Application US/08482279
Sequence 10: Sequence 69, Application US/0848279
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods TITLE OF INVENTION: Of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS: 70
CORRESPONDENCE ADDRESS: 70
CORRESPONDENCE ADDRESS: 70
CORRESPONDENCE ADDRESS: 70
CORPUTER: Canifornia
COMPUTRY: USA
ZIP: 92122
COMPUTRY: USA
ZIP: 92122
COMPUTRY: USA
ZIP: 92122
COMPUTRY: USA
ZIP: 92124
COMPUTRY: USA
ZIP: 92124
COMPUTRY: USA
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COMPUTRY: USA
ZIP: 92124
COMPUTRY: USA
ZIP: 92127

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62.5%; Score 25; DB 1; Length 2408;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 25; Conservative 0; Mismatches 0; Indels
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TELEPAK: (619) 535-9001
TELEPAK: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
                                             2408 base pairs
                                                                                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-486-013-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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US-08-482-279-69
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| Patent No. 573149 |
| Patent No. 573149 |
| GENERAL INFORMATION: |
| APPLICANT: Seleted, Michael E. |
| APPLICANT: OHellette, Andre J. |
| TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods |
| TITLE OF INVENTION: of Their Use |
| NUMBER OF SEQUENCES: 70 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Campbell and Flores |
| STREET: 4370 La Jolla Village Drive, Suite 700 |
| CITY: San Diego |
| STATE: California |
| STATE: California |
| COUNTRY: USA |
| TITLE OF INVENTION |
| TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 25; DB 1; Length 201; 100.0%; Pred. No. 0.38; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24 FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGIGTRATION NUMBER: 520.31930X00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-666
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDENBESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
HYPOTHETICAL: YES
HYPOTHETICAL: YES
HYPOTHETICAL: YES
HYPOTHETICAL: YES
HYPOTHETICAL: YES
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUN
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Best Local Similarity 100.
Matches 25; Conservative
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US-08-728-785A-18
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US-08-486-013-69
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US-09-015-968-69
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US-09-015-968-69
Sequence 69, Application US/09015968
Patent No. 6057425
Harin No. 6057425
TERRAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: Of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
Sequence 2007. Application US/08342268

Sequence No. 5844072

GENERAL INFORMATION:

APPLICANT: Seleted, Michael E.

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods

TITLE OF INVENTION: Of Their Use

TITLE OF INVENTION: Of Their Use

TORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: San Diego

CITY: San Diego

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 2408; 0.56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: 10-NOV-1994
CLASSIPICATION 1435
PRIOR APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATPONEY/AGENT INPORMATION:
NAME: Campbell, Cathyr, A
REGISTRATION NUMBER: 31,815
REBERENCE/DOCKET NUMBER: 31,815
REBERENCE/DOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 25; DB 100.0%; Pred. No. 0.5 Live 0; Mismatches
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Best Local Similarity 100.'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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US-08-342-268-69
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WORDTIER: IMP PEC COMPATIBLE
OWNETHER: IMP PEC COMPATIBLE
OWNETHER: IMP PEC COMPATIBLE
OWNETHER: IMP PEC COMPATIBLE
OF COMPATIBLE
PELICATION NATIBLE
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PELICATION NATIBLE
PERIOR APPLICATION NATIBLE
PERIOR PELICATION NATIBLE
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PERIOR PE
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us-10-082-772-2.rni

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STATE: BOSCHUSELTS

COUNTRY: United States

ZIP: 02109

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/380,090A
FILING DATE: 17-May-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION SOFTWER: WO PCT/EP97/06472
FILING DATE: 18-NOV-1997
APPLICATION NUMBER: WO PCT/EP97/06472
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: SUBERKO, COlleen
REGISTRATION NUMBER: 39,850
TELECOMMUNICATION NUMBER: 39,850
TELEBROCE/DOCKET NUMBER: SYN-010
TELEBROCE/OCKET NUMBER: SYN-010
TELEBROCE/OCKET NUMBER: SYN-010
TELEBROCE/OCKET NUMBER: SYN-010
                                                                                                                                                                                                                                                                                                            KLAP, JOKE
TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             )
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-380-090A-1
                                                                            Sequence 1, Application US/09380090A
Patent No. 655529
GENERAL INFORMATION:
APPLICANT: OHL, Stephan Andreas
KLEIN-VAN DER LEE, Frederique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CREANISM: Arabidopsis thaliana
STRAIN: C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP STREET: 60 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCE CHARACTERISTICS:
LENGTH: 3484 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relefax: (617) 526-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
3481..3484
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                                                                                                                                                                                                                                                                                                         GODDIJN,
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                                                      JS-09-380-090A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09308090
| Patent No. 6395963
| GENERAL INFORMATION; Stephan APPLICANT: Ohl, Stephan APPLICANT: Ohl, Stephan APPLICANT: Ohl, Stephan APPLICANT: Van Der Lee, Frederique APPLICANT: Klap, Joke APPLICANT: Rimons, Peter ITILE OF INFORTION; Nematode-Inducible Regulatory DNA Sequences; TILE OF INFORTION; Nematode-Inducible Regulatory DNA Sequences; FILE REFERENCE: MOG 5'560; CURRENT FILING DATE: 1999-05-14
| EARLIER PILING DATE: 1999-05-14
| EARLIER FILING DATE: 1997-11-18
| MUMBER OF SEQ ID NOS: 10
| SOFTHARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
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Pred. No. 0.6;
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APPLICATION NUMBER: US 08/482,279
PRIOR PAPPLICATION NUMBER: US 08/482,279
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-UC 3003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.(
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: (3482)..(3484)
US-09-308-090-1
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LENGTH: 3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-397-386-69
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Query Match 62.5%; Score 25; DB 4; Length 3484; Best Local Similarity 100.0%; Pred. No. 0.6; Matches 25; Conservative 0; Mismatches 0; Indels soz rcartartrgartrcaartrrgrcc ssi 16 TCATTATTTGATTTCAATTTTGTCC 40

RESULT 12 US-09-016-366A-13

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Gaps
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Pred. No. 0.6;
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US-08-556-978B-78/c
Sequence 78, Application US/08556978B
Patent No. 6288169
GENERAL INFORMATION:
APPLICANT: FAPRINESTOCK, STEPHEN F.
TITLE OF INVENTION: SPIDER BILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCES: 107
ADDRESSES: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINTON
STATE: DELAMARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 1989B
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
         FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                              CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/978,404B
APPLICATION WMBER: US/08/978,404B
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04-DEC-1996
ATTORNEY AGENT INFORMATION:
NAME: Plumer, Blizabeth R.
REGISTAATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEFAX: 617-720-3500
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTONEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TCATTATTTGATTTCAATTTTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3757 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 302-1,
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
TWATH: 4909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4909 base |
TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-978-404B-19
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Patent No. 5968782
GENERAL INFORTION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                              GENERAL NO. 3202431
GENERAL NO. 3202431
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: ANDIT OF SECUENCES: 65
CONTEXT: 600 Atlantic Avenue
STREET: 600 Atlantic Avenue
CITY: Boston
STREET: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EactSEQ for Windows Version 2.0
COMPUTER: IBM Compatible
OPPERATION NUMBER: 05/09/016,366A
FILING DATE: 05 FEB-1997
ATTORNEY APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05 FEB-1997
ATTORNEY ACENT INFORMATION:
NAME: PLUMEY: Elizabeth R:
REGESTRATION NUMBER: 36,637
REGESTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Sequence 13, Application US/09016366A
Patent No. 5955431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORREST.

ADDRESSE: Wolf, Greenier STREET: 600 Atlantic Avenue CITY: Boston STATE: MA COUNTRY: U.S.A. ZIP: 0.2211 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette MEDIUM TYPE: Diskette TREADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH 3757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear / MOLECULE TYPE: CDNA US-09-016-366A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-08-978-404B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
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NAME/KEY: misc feature

LOCATION: Complement ((98) .. (331))

OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"

OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"

OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"

OTHER INFORMATION: label = bar, "region coding for phosphinthricin OTHER INFORMATION: acetyl transferase"

FEATURE:

NAME/KEY: misc feature

LOCATION: Complement ((884) .. (2258))

OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic OTHER INFORMATION: Virus."
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (4246). (4577)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: 13060)..
OTHER INFORMATION: 92/13956)..
NAME/KEY: misc feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: 1abel = synb*; "improved barstar DNA"
                                                                                                                                                                 0
                                                                                                        Query Match 62.5%; Score 25; DB 3; Length 4909; Best Local Similarity 100.0%; Pred. No. 0.63; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: Label = RB, "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
! CCATION: Complement ((5325)..(5349))
! OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-068-101-7
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09068101
Patent No. 6372960
GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TILLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2121-139P
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
BARLIER FILING DATE: 1996-09-03
NUMBER: OSEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 5349
LENGTH: 5349
                                                                                                                                                                                                                                                       2288 TCATTATTTGATTTCAATTTTGTCC 2264
                                                                                                                                                                                                            16 TCATTATTTGATTTCAATTTTGTCC 40
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-068-101-7/c
                                                                                                                                                                                                               ò
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Query Match 62.5%; Score 25; DB 4; Length 5349;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 16 TCATTATTTCAATTTGTCC 40
Db 4798 TCATTATTTCAATTTGTCC 4774
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Search completed: December 3, 2003, 14:51:45 Job time : 48.6033 Becs

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RESULT 2
US-09-981-002-25
; Sequence 25, Application US/09981002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
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Sequence 72, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 113, Appl
Sequence 7, Appl
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Appl
Sequence 3194, Ap
Sequence 3198, Ap
Sequence 46, Appl
Sequence 5700, Ap
Sequence 5700, Ap
Sequence 20518,
                                                                                                                              December 3, 2003, 13:18:51; Search time 178.512 Seconds (without alignments) 744.732 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                           1 aaggaaagcggccgctcattatttgatttcaattttgtcc 40
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-082-772-2
US-09-981-002-25
US-09-244-805-57
US-09-245-277-57
US-09-245-277-57
US-09-970-921-10
US-09-970-921-10
US-09-970-921-10
US-09-970-921-10
US-09-970-921-10
US-09-970-921-10
US-09-970-921-10
US-09-970-981-803-37
US-09-981-803-37
US-09-991-803-37
US-09-991-803-37
US-09-991-803-37
US-09-991-803-37
US-09-974-300-570618
US-10-027-632-206518
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                         2201672 segs, 1661799599 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Applications NA:
                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                  IDENTITY NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-082-772-2
40
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228821
22883446
228834463
22883446
2228
330
6750
6788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
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c 17 22.2 55.5 678 12 US-10-027-632-206520 Sequence 206520, c 18 22.2 55.5 678 13 US-10-027-632-206521 Sequence 206521, c 20 22.2 55.5 678 13 US-10-027-632-206529 Sequence 206521, c 21 22.2 55.5 678 13 US-10-027-632-206529 Sequence 206521, c 22 22.2 55.5 678 13 US-10-027-632-206520 Sequence 206521, c 22 22.2 55.5 2541 13 US-10-027-632-206522 Sequence 206522, c 24 22.2 55.5 2541 13 US-10-027-632-206522 Sequence 206522, c 24 22.2 55.5 2541 13 US-10-027-632-206522 Sequence 206522, c 24 22.2 55.0 38 9 US-10-161-403-37 Sequence 206522, c 25 25.0 1071 14 US-10-161-403-37 Sequence 206522, c 27 22 55.0 1071 14 US-10-161-403-37 Sequence 206522, c 28 22 55.0 5855 14 US-10-161-403-37 Sequence 112, Application of the color of the color
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## ALIGNMENTS

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                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: Primer US-10-082-772-2
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                                                                                                                                                                                                                                                  Length 40
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                AAGGAAAGCGGCCGCTCATTATTTGATTTCAATTTTGTCC
                                                                                                                                                                                                                                                                                     1 AAGGAAAGCGCCCCCTCATTATTTGATTTTCAATTTTGTCC
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                100.0%; Score 40; DB 14; 100.0%; Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 40; Conservative
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US-09-245-277-57/C

US-09-245-277-57/C

I Gequence 57, Application US/09245277

Publication No. US20030211984A1

GENERAL INFORMATION:

APPLICANT: Worldy, Paul F.

APPLICANT: Lanahan, Anthony

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: IMMEDIATE

TITLE OF INVENTION: IMMEDIATE

TITLE OF INVENTION: UNMERR: US/09/245,277

CURRENT FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: 60/074,135

PRIOR APPLICATION NUMBER: 60/074,135

PRIOR PILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: 1763
                                                               APPLICANT: Worley, Paul F.
APPLICANT: Gorez, Bernard
APPLICANT: Lanahan, Anthony
APPLICANT: Gorez, Bernard
APPLICANT: Gorez, Bernard
APPLICANT: Kuner, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Shukovski, Eugene
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: IMMEDIATE 1999-02-05
EARLIER APPLICATION NUMBER: 60/074,518
EARLIER APPLICATION NUMBER: 60/074,135
EARLIER FILING DATE: 1998-02-06
SOFTWARE: FASTES OF TO WINGHER: 60/074,135
EARLIER FILING DATE: 1998-02-06
SOFTWARE: FASTES OF TO WINGHOUS VERSION 4.0
SEQ ID NO 57
LENGTH. 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 25; DB 12;
100.0%; Pred. No. 11;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%; Score 25; DB 12;
100.0%; Pred. No. 11;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | LOCATION: (1)._.(1763)
| OTHER INFORMATION: y = C or T
| CTHER INFORMATION: n = A,T,C or G
US-09-244-805-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | LOCATION: (1)...(1763)
| OTHER INFORMATION: Y = C or T
| OTHER INFORMATION: n = A,T,C or G
| US-09-245-277-57
           US20030203840A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Bukaryote
FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Eukaryote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                       | APPLICANT: TAKARA SHUZO CO., Ltd. | APPLICANT: TAKARA SHUZO CO., Ltd. |
| TILLE OF INVENTION: DNA POLYMERASES WITH ENHANCED LENGTH OF PRIMER EXTENSION |
| TILLE OF INVENTION: DNA POLYMERASES WITH ENHANCED LENGTH OF PRIMER EXTENSION |
| TILLE OF INVENTION: TAKASOO.1 |
| CURRENT APPLICATION NUMBER: US 08/021,623 |
| PRIOR APPLICATION NUMBER: US 08/021,623 |
| PRIOR PAPLICATION NUMBER: US 08/483,535 |
| PRIOR PAPLICATION NUMBER: US 08/483,535 |
| PRIOR PELING DATE: 1992-06-07 |
| PRIOR PELING DATE: 1997-09-16 |
| NUMBER OF SEQ ID NOS: 29 |
| SOFTWARE: PALENTIN VETSION 3.0 |
| SEQ ID NO 25 |
| LENGTH: 33 |
| WALLET OF THE OFFICE OFFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; Score 25; DB 11; Length 33; llarity 100.0%; Pred. No. 4.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 282
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100.0%; Pred. No. ...
0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 rcarraringarricaarrirgic 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
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US-09-244-805-57/c
. Sequence 57, Application US/09244805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TCATTATTTGATTTCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Bacteriophage lambda
US-09-981-002-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
Publication No. US20030049634A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: attp
US-10-161-403-72
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Best Local Similarity
Matches 25, Conserv?
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Gaps

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Gaps

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OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "plasmid pLH48"

OTHER INFORMATION: acid, "plasmid pLH48"

NAME/KEY: misc feature

OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium OTHER INFORMATION: T-DAA"

NAME/KEY: misc feature

LOCATION: Complement (318)..(869)

OTHER INFORMATION: acetyl transferase"

NAME/KEY: misc feature

LOCATION: Complement (670)..(1702)

OTHER INFORMATION: acetyl transferase"

LOCATION: Complement (670)..(1702)

OTHER INFORMATION: Jabel = P35S, "35S promoter of Cauliflower Mosaic OTHER INFORMATION: Virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1740)..(2284)
OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INCOMPLEMENT OF STANDARD OF STANDARD
                                                                                                   NAME/KEY: misc feature
LOCATION: Complement((884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: virus"
NAME/KEY: misc feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
OTHER INFORMATION: 92/13956)"
                                 OTHER INFORMATION: label = bar, "region coding for phosphinthricin OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%; Score 25; DB 10; Length 5349; 100.0%; Pred. No. 14; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (2285)..(2560)
OTHER INFORMATION: label = synb*, "improved barstar DNA"
NAME/KEY: misc feature
LOCATION: (2561)..(2892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // LOCATION: Complement((5325)..(5349))
// OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09970921
Patent No. US20020133845A1
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: 5611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4798 rcarrarricarricaarrirgrec 4774
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Complement ((332).. (883))
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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US-09-970-921-10/c
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NAME/KEY: misc feature

LOCATION: COMplement((1)..(25))

OTHER INFORMATION: label = RB, "T-DNA right border"

NAME/KEY: misc feature

LOCATION: Complement((98)..(331))

OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"

NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PETALLA, ELWALL
APPLICANT: PETEZ, CATA
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Elwing, Elena
APPLICANT: Stewart, Sandra
APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2002-03-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 113
LENGTH: 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: pSV40-193AttpsensePur Plasmid
US-10-161-403-113
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Patent No. US20020133845a1
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Barstar Gene
FILE RERERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4298 rcarrarridarricaarrirgicc 4322
                                                                                                   203 rcarrarraarracaarrarca
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                                                                                                                                                                                                                                                                                                       Sequence 113, Application US/10161403; Publication No. US20030119104A1; GENEAL INFORMATION: APPLICANT: Perkins, Edward; APPLICANT: Perez, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Conserva
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US-09-970-921-7/c
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FEATURE:

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Sequence 3194, Application US/09764877
Fatent No. US20020147140A1
GENERAL INFORMATION:
TILLS INFORMATION:
TILLE OF INVENTION: NUMBER: US/09/764,877
CURRENT PELLOATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3194
LENGTH: 28313
                                                                                                                                                                                                                                                                                                  Score 22.6; DB 10; Length 28313;
Pred. No. 1.7e+02;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                          1 AAGGAAAGCGCCGCTCATTATTTGATTTCAATTTTG 37
                                                                                                                                                                                                                                                                                                       56.5%;
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                   Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Weld, Rod
TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coli 0157
CORRESPONDENCE ADDRESS:
) OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated ; OTHER INFORMATION: end of chalcone synthase gene" US-09-970-921-10
                                                                                                       Gaps
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                                                                   Length 5611;
                                                                                                     0; Indels
                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                   62.5%; Score 25; DB 100.0%; Pred. No. 14; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-114-170-50
                                                                                                                                                                     3113 rchrhirdahrrcharrrigicc 3089
                                                                                                                                                                                                            RESULT 9
US-10-114-170-50
i Sequence 50, Application US/10114170
i Publication No. US20030023075A1
i GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Rurland, ..., melenie
                                                                                                                                  16 TCATTATTTGATTTCAATTTTGTCC 40
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS
                                                               Query Match
Best Local Similarity 100.(
Matches 25, Conservative
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Best Local Similarity
Matches 25; Conserva
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Gaps

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Sequence 37, Application US/09981803

Publication No. US20030032092A1

GENERAL INFORMATION

APPLICANT: Daniel SCHERMAN

APPLICANT: Beatrice CAMERON

APPLICANT: Beatrice CAMERON

APPLICANT: Anne-Marie DARQUET

ITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY

FILE REFERENCE: MINICIRCLE

CURRENT APPLICATION NUMBER: US/09/981,803

CURRENT PILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 37

LENGTH: 30
                                                                                                                                             Sequence 3198, Application US/09764877

Patent No. US20020147140A1

GENERAL INCORNATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-7

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3198

LENGTH: 29228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.5%; Score 22.6; DB 10; Length 29228; Best Local Similarity 75.7%; Pred. No. 1.78+02; Matches 28; Conservative 0; Mismatches 9; Indels 0:
16691 AAGGAGAAGGGCTGCTCATCACCTGATTACCATTTTG 16655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14237 AAGGAGAAGGGCTGCTCATCACCTGATTACCATTTTG 14201
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RESULT 10

Gaps

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Indels

0; Mismatches 11;

136 AACGATATCGCCAGCTGAAATTTGCTTTCAATGTTTTCC 1 AAGGAAAGCGGCCGCTCATTATTTGATTTCAATTTTGTCC

Length 450;

DB 10;

56.0%;

29; Conservative

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Search completed: December 3, 2003, 17:22:24
Job time : 180.512 secs
                                             Best Local Similarity Matches 29; Conserva
                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Daniel SCHERMAN
APPLICANT: Beatrice CAMERON
APPLICANT: Pierre WILS
APPLICANT: Anne-warie DAROUBT
TITLE OF INVENTION: DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
FILE REPERENCE: MINICIRCLE
CURRENT APPLICATION NUMBER: US/09/981,803
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 30
TYDE
                                                                                                                                                                                                      Gaps
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Fatent No. US20020146721A1
GENERAL INCRMATION:
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-07
SOFTWARE OF SEQ ID NOS: 8481
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 5700
                                                               OTHER INFORMATION: Description of the artificial sequence:
OTHER INFORMATION: oligonucleotide
US-09-981-803-37
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of the artificial sequence:
OCHER INFORMATION: oligonucleotide
US-09-981-803-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                    Query Match 56.0%; Score 22.4; DB 11; Best Local Similarity 95.8%; Pred. No. 40; Matches 23; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.0%; Score 22.4; DB 11; Best Local Similarity 95.8%; Pred. No. 40; Matches 23; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                        7 GGPCATTATTTGATTTCAATTTTG 30
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US-09-981-803-46
Sequence 46, Application US/09981803
Publication No. US20030032092A1
GENERAL INFORMATION:
APPLICANT: Joel CROUZET
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
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US-09-974-300-5700/c
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Sequence 206518, Application US/10027632

Publication No. US20030204075A9

Publication No. US20030204075A9

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

PRIOR PELING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

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PRIOR FILING DATE: 1999-11-23

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PRIOR FILING DATE: 1999-09-28

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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGGAAAGCGCCCCTCATTATTTGATTTCAATTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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COTHER INFORMATION: n = A,T,C or G
US-10-027-632-206518
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Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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NF092E03I WHE2457 Rfc00051 Rfc01922 EST533345

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

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Run

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BE43508 BE370513

AQ990513 Rfc01299

AQ990131 Rfc01295

AQ991241 Rfc02132

AQ99132 Rfc01894

AQ991352 Rfc01894

AQ990346 Rfc01106

AQ990346 Rfc01106

AQ990346 Rfc01106

AQ990310 Rfc00127

AQ990310 Rfc01055

AQ990310 Rfc01055

AQ990310 Rfc01153

AQ990310 Rfc01153

BNS33719 fw96d12.y

AQ99038 Rfc01153

BNS33719 fw96d12.y

AQ99078 Rfc01579

BNS33719 fw96d12.y

AQ99078 Rfc01579

BNS3719 AGECOUTF

AQ99078 Rfc01579

BNS3719 AGECOUTF

AQ59078 AGECOUTF

AQ5908 AGECOUTF

AQ5908 AGECOUTF

AQ5908 AGECOUTF

AQ5908 AGECOUTF

AQ5908 AGECOUTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
gurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago.

1 (Dases 1 to 206)

1 Torres-Jeres, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula irradiated library
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 bp mRNA linear EST 24-NF092F0ZIR1F1027 Irradiated Medicago truncatula cDNA clone
                                                    BG312744 W
AQ989502 B
AQ991064 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: May GD
Plant Blology Division
Plant Blology Division
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Email: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                       BE435088
AQ990513
AQ990813
AQ991241
AQ991039
AQ991039
AQ990173
AQ990170
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AQ990170
AQ990301
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AQ990758
BH730850
BH544112
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CB292689
CNSOINCR
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AQ664509
BB624763
BM804116
CB092932
                                   BQ156404
BG312744
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BQ156416.1 GI:20293475
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BQ156416 NF092F021
AU244794 AU244794
BQ156182 NF090A021
AQ991303 R£G02205
                                                                                                                December 3, 2003, 12:13:45; Search time 1793.72 Seconds (without alignments) 541.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                               45562784
                                                                                                                                                                                                                                  1 aaggaaagcggccgctcattatttgatttcaattttgtcc
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                - nucleic search, using sw model
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AU244794
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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6: em_esthu::*
7: em_estpl::*
10: gb_estp::*
11: gb_estp::*
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Match Length DB
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BQ156182/c
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                                                                                                                                                                                         /tissue_type="seedlings"
/dev_stage="seedlings"
/dev_stage="seedlings"
/dev_stage="seedlings"
/clone_lib="tradiated"
/clone_lib="tradiated"
/none_lib="tradiated amplea Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XII-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU244794 Shibata Xenopus ABM lambda-ZAP II cDNA library Xenopus laevis cDNA clone p6e6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus; Mesobatrachia; Pipoidea; Buteleostomi; 1 (bases 1 to 360)
Shibata,M., Itoh,M., Ohmori,S., Shinga,J. and Taira,M.
Systematic screening and expression analysis of the head organizer per in Xenopus embryos
Dev. Biol. 239 (2), 241-256 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Far: 81-03-5841-4434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: m taira@biol.s.u-tokyo.ac.jp,
URL:http://www.biol.s.u-tokyo.ac.jp/users/lmb/lmb-hp.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%; Score 25; DB 13; Length 206; 100.0%; Pred. No. 6.4e+02; ive 0; Mismatches 0; Indels
                                                                                  1. .206
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/db xref="taxon:3880"
/clone="NF092F02IR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 t
  Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
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/clone="p6e6"
Insert Length: 206 Std Error: 0.0
Plate: 092 row: F column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                Location/Qualifiers
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AU244794
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                                                                FEATURES
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g 8

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//do_xere="mena"
//do_xere="mena"
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//tissue_type="seedlings"
//dow stage="seedlings"
//dow gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
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total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Giappack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XL1-Blue MRF,
//dow stragene). Excised plasmids were plated using SOLR
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NF090A02IR1F1017 Irradiated Medicago truncatula cDNA clone
NF090A02IR 5', mRNA sequence.
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Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
; eurosids I; Fabales; Fabaceae, Papilionoideae, Trifolieae,
/tissue_type="anterior endomesoderm"
/dev_stage="late gastrula to early neurula stages 12.5-13"
/clone_lib="Shibata Xenopus AEM lambda-ZAP II cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Stores,H.K., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Term the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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                                                                                                                                                                                                                                   Length 360;
                                                                                                                                      2 others
                                                                                                                                                                                                                                                                                                     0; Indels
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 388 Std Error: 0.00
Plate: 090 row: A column: 02
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                   Score 25; DB 9; Le
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                Query Match 62.5%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 6.1 Matches 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                16 TCATTATTTGATTTCAATTTTGTCC
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BQ156182.1 GI:20293229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago.
1 (bases 1 to 388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 C
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

RESULT 4 AQ991303/c DEFINITION

Matches

g

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/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum. Total RNA, and poly(A) RNA were prepared and pooled from infected spike at 0, 6, 12, 24, 36 and 48 hours after inoculation, a CDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in G. Muchlbauer lab at the University of Minnesota (Kruger, W.M., Muchlbauer, G.U., Pritsch, C., Vance, C.). The CDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
West Area, Western Regional Research Center
West Sions Street, Albany, CA 94710, USA
Tel: 510559573
Fax: 510559573
Fax: 51055957818
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST seq primer: Stratagene SK primer.
                                                                             Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryoty, Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Triticum aestivum".
/mol type="mRNA"
/mol type="mRNA"
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/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
/clone_lib="Wheat Fusarium graminearum infected spike cDNA
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NF104D07IR1F1062 Irradiated Medicago truncatula cDNA clone
NF104D07IR 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    the structure and function of the expressed portion of the wheat genomes - Fusarium graminearum infected spike cDNA library Unpublished
                                                                                                                                                                                                                     1 (bases 1 to 417)
Anderson,O.D., Chao,S., Han,P.S., Heinen,S., Hsia,C.C., Kang,Y.,
Kruger,W.M., Lazo,G.R., Miller,S., Muehlbauer,G.J., Miller,R.,
Pritsch,C., Rausch,C.J., Seaton,C.L., Tong,J.C., Vance,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula (barrel medic)
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                                    GI:17141863
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Best Local Similarity
Matches 25; Conservat
                              VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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LOCUS
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
baborn, P.J., Bowen, D. and Blattner. P.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM134283 417 bp mRNA linear EST 28-NOV-20
WHE0488_B03_C06ZS Wheat Fusarium graminearum infected spike cDNA
library Triticum aestivum cDNA clone WHE0488_B03_C06, mRNA
                                                                                                                                                                                                                                                                                           AQ991303 Rfc02205 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens clone PLG02205, genomic survey
                                                          Gaps
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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                              6.1e+02;
hes 0;
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100.0%; Pred. No. 6.1e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Buildling, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                           Pred. No. 6.1); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                        171 rchrinitrichiricharrirerce 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:29488"
/clone="PLG02205"
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                                                                                                         16 TCATTATTTGATTTCAATTTTGTCC 40
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Class: shotgun.
Location/Qualifiers
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                       AQ991303
AQ991303.1 GI:9649897
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Best Local Similarity 100.0
Matches 25; Conservative
                                                    Conservative
                        Best Local Similarity
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DEFINITION

ACCESSION

RESULT 5 BM134283

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BASE COUNT

ORIGIN

FEATURES

TITLE

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/tissue type="seedlings"
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/clone_lbb="ltradiated"
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/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coll strain XII-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago, truncatula irradiated library
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                                             Moublished Contact Interaction Interaction of Contact: May GD Plant Balogy Division 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Test: 580 221 7391 Email: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 13;
Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%; bcc.
100.0%; Pred. No. c.
... 0; Mismatches
                                                                                                                                                                                                                Email: gdmay@noble.org
Insert Length: 473 Std Brror: 0.00
Plate: 092 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF092E031R"
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BG312744.1 GI:13114547
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Triticum monococcum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                         FEATURES
     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="seedings" / dev surface: Lambda 229; Seedings were exposed either to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation. Gamma-irradiated samples were harvested at 6, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. CDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coll strain XLI-Blue MRF. (Stratagene). Excised plasmids were plated using SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 bp mRNA linear EST 24-APR-2002
NF092E03IR1F1023 Irradiated Medicago truncatula cDNA clone
NF092E03IR 5', mRNA sequence.
BQ156404.1 G1:20293463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
; eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
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                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7381
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 472 Std Brror: 0.00
Plate: 104 row: D column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.

ce 1. .472
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="NF104D07IR"
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     Medicago truncatula
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Best Local Similarity
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BQ156404/c
     ORGANISM
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AUTHORS
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FEATURES

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/db_xref="taxon:29488"
/clone="PLG00051"
/clone="pLG00051"
/clone lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae, Photorhabdus.

1 (bases 1 to 587)

1 (bases 1 to 587)

1 (bases 1 to 587)

2 (bases 1 to 587)

2 (bases 1 to 587)

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Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ991064 11near GSS 14-AUG-2
Rfc01922 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01922, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 25; DB 28; Length 572;
100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/strain="W14"
                                                                                                                    /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 TCATTATTTGATTTCAATTTTGTCC 510
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/clone="PLG01922"
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      Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
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Class: shotgun.
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Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="watch: 1500"
/tissue_type="marry reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. col; Xwolk"
/lab_host="E. col; Xwolk"
/clone lib="Triticum monococcum early reproductive apex
cDNA library:
/clone lib="Triticum monococcum early reproductive apex
cDNA library:
/note="Wetor: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: Xhol; The tissue, total RNA, and
poly/Ah RNA were prepared from apex at double-ridge stage
to terminal-spikelet stage during transition from
vegetative state to flower state, a cDNA library was made,
and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky): Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Department of Biology and Blochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For
This is one of 2.122 random ceads from the M13 library of Scotial K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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Enterobacteriaceae; Photorhabdus,
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Rfc00051 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00051, genomic survey
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                                                             Fax: 5105595818
Email: candersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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Buchanan Street, Albany, CA 94710, USA
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100.0%; Pred. No. 5.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   organism="Triticum monococcum"
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                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="DV92"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other authors)
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1 (bases 1 to 641)
fixench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Phocorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamidis, Solanales, Solanaceae, Solanum, Lycopersicon. 1 (bases 1 to 622)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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/dev_stage="breaker"
/dev_stage="breaker"
/clone_lib="tomato breaker fruit, TIGR"
/clone_lib="tomato breaker fruit, TIGR"
/clone_lib="tomato breaker fruit, TIGR"
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Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
143 c 145 g 166 t
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Rfc01299 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01299, genomic survey
sequence
AQ990513
                                                                                                                                                                                                                                Generation of ESTs from tomato fruit tissue, breaker stage Unpublished
                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
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Department of Biology and Biochemistry
University of Bath
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clone="cLEG25A5"
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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Best Local Similarity 100.0
Matches 25; Conservative
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/dev_stage="15-40 days old"
/lab_host="x11-Blue MRF""
/clone_lib="tomato callus, TAMU"
/clone_lib="tomato callus, TAMU"
/clone_lib="tomato callus, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Giovannoni laboratory; clac - Cotyledons
of, seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                         EST533345 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC71G2 5' end, mRNA sequence.
B1422679.1 GI:15197297
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Lycopersicon esculentum
Eukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solamales; Solamaceae, Solanum; Lycopersicon.

[ Dases 1 to 597)
Alcala,J., Virbala,O.,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Roming
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
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100.0%; Pred. No. 5.9e+02;
iive 0; Mismatches 0; Indels
                                                   Length 587;
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                                              62.5%; Score 25; DB 28; I
100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
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Class: shotgun.
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Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proceobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 664)
ffrench-Constant, F.H., Waterfield, N., Burland, V., Perna, N.T.,
ffrench-Constant, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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145 c 158 g 170 t
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: shorgun.
Location/Qualifiers
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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Rfc01864 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01864, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/clone_lib="Photorhabdus luminescens strain W14 M13
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1. 641
/organism="Photorhabdus luminescens"
/srgutype="genomic DNA"
/strain="W14"
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="M14"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG01864"
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/clone="PLG01299"
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AQ991011.1 GI:9649605
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(farench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
146 c 162 g 175 t 3 others
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Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.
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Rfc01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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1 Similarity 100.0%; Pred. No. 5.8e+02;
25; Conservative 0; Mismatches 0; Indels
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146 c 161 g 179 t 2
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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Search completed: December 3, 2003, 14:49:16 Job time: 1796.72 secs

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Score
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                                                                  2003, 12:13:45; Search time 652.562 Seconds (without alignments) 1504.579 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AX022116 Sequence
AX044609 Sequence
BC5439 Oligonucleo
I13139 Sequence 18
AX09213 Sequence
AX08213 Sequence
BX3641 Bacteriopha
AX09213 Sequence
DB5521 Macaca fasc
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AX04872 CRIM plas
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U39286 Cloning vec
U39286 Cloning vec PAT 21-MAR-2001 score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence-specific dna recombination in eukaryotic cells Patent: WO 0116345-A 5 08-MAR-2001; Droege, Peter (DE) linear DNA ALIGNMENTS SUMMARIES AXO92116 243 bp Sequence 5 from Patent WO0116345. AXO92116 GI:13444359 E05439 113139 136498 AX092113 LAMINTATT AX101000 AX370644
AX113747
AX113747
AY150266
AY048713
AY048739
AY1778451
AP065529
CVU39284
CVU39285
CVU39285
CVU37692 artificial sequences В synthetic construct synthetic construct Query Match Length 3695 4105 4190 4549 4549 47849 5911 5948 5986 6000 Droege, P. REFERENCE AUTHORS TITLE JOURNAL

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Gaps

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PAT 26-JUL-1995
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1 (bases 1 to 201)

1 (bases 1 to 201)

Separation of polynuclectides using supports having a plurality of electrode-containing cells
Patent: US 5434049-A 18 18-JUD-1995;

Location/Qualifiers
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1 (bases 1 to 201)
Okano, K. and Kambara, H.
Device for separating polynucleotides having a plurality of electrode-containing calls and movable collecting capillary Patent: US 5607646-A 18 04-MAR-1997;
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/organism="synthetic construct"
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Sequence 18 from patent US 5434049.
113139.1 GI:910488
                                                                                             Query Match 93.3%; Score 22.4; I
Best Local Similarity 95.8%; Pred. No. 42;
Matches 23; Conservative 0; Mismatches
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93.3%; Score 22.4; I
Best Local Similarity 95.8%; Pred. No. 42;
Matches 23; Conservative 0; Mismatches
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Pred. No. 42;
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Unknown.
Unclassified.
Unclassified.

1 (bases 1 to 201)
Okano, K. and Kambara, H.
Polymuclectide capturing support for capturing, eluting and collecting polynucleotides in a sample solution
Patent: US 5817506-A 18 06-0CT-1998;
Location/Qualifiers
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                                                                                                                      100.0%; Score 24; DB 6; Length 243; 100.0%; Pred. No. 8.5; 0; Indels ive 0; Mismatches 0; Indels
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synthetic construct
artificial sequences.
1 (bases 1 to 201)
Okano, K. and Kanbara, H.
CHIP FOR CATCHING POLYNUCLECTIDE
Patent: JP 1993236997-A 11 17-SEP-1993;
HITACHI LTD
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Artificial sequence; Genes.
Dr 1993236997-A/11
17-SEP-1993
28-FEB-1992 JP 1992042829
OKANO KAZUNOBU, KANBARA HIDEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.3%; Score 22.4; I
Best Local Similarity 95.8%; Pred. No. 42;
Matches 23; Conservative 0; Mismatches
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strandedness: Single;
topology: Linear.
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JP 1993236997-A/11.
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Best Local Similarity 100.
Matches 24; Conservative
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E05439
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MACHSS 166B bp mRNA linear PRI 06-FEB-1999
Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
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                        PAT 10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of Pharmacy and Life Science, Department of Drug Metabolism and Molecular Toxicology: 1432-1 Horinouchi, Hachioji, Tokyo 192-0392, Japan (E-mail:ogurak@ps.tcyaku.ac.jp, Tel:+81-426-76-4518, Location/Qualifiers
                                                                                                                               Nicotiana tabacum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydroxysteroid sulfotransferase subunit.
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis (braniaris) (braniaris) (butebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniara; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Ogura,K., Satsukawa,M., Kato,K., Okuda,H. and Watabe,T.
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
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                                                                                                                                                                                                                     Meyer, P.L. and Zubko, E.L.
Targeted gene removal
Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
Location/Qualifiers
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                                                                                                                Nicotiana tabacum (common tobacco)
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AX101000.1 GI:13619857
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2 (bases 1 to 1668)
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Best Local Similarity 95.8
Matches 23; Conservative
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Machinates, no RNA stage, Caudovirales, Siphoviridae, Lambda-like viruses.
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                                                                                                                                                                                Bacteriophage lambda
Bacteriophage lambda
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                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bacteriophage lambda"
/mol_type="genomic DNA"
/db_xref="taxon:10710"
/ 34 c 33 g 102 t
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/mol_type="genomic DNA"
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                                                                                         AX092113 243 bp Sequence 2 from Patent W00116345.
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Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum (malaria parasite P. falciparum)
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Plasmodium falciparum
1 (bases 1 to 2758)
Lenstra, R., d'Auriol, L., Andrieu, B., Le Bras, J. and Galibert, F.
Cloning and sequencing of Plasmodium falciparum DNA fragments
containing repetitive regions potentially coding for histidine-rich
proteins: identification of two overlapping reading frames
Blochem. Blophys. Res. Commun. 146 (1), 368-377 (1987)
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/protein_id="AAA29619.1"
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/translation="MLNHRYHHYFHRHHHLNHHLYHRHHHRHHHRHQILHQN
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KKEPLERKRDEIIQKIPGFWANTLRKHPALSDIVPEDIDILNHUVKLDLKDNMONNGS
YKITFIFGEKAKETRELGITUKHVYTPDNQEKVVECTRIKWKGKNPIAAVTHNRSDL
DNEIPWKSIPEWFTPDELQDKPDVGELIRREIMHPLSYYLGIEEFDEFDDEFD
               QLFPKSFFSSKAKVIYLMRNPRDVFVSGYFFMNSVKFVKKPKKMQQYFEWFCQGNVIY
GSWFDHIHGWMPMREKKNFLLLSYEELKQDTRRTVEKICQFLGKTLEPEELNLILKNS
SFQSMKENKMSNFSLLSVDFVFEKAQLLRKGISGDWRMHLTVAQAEAFDKLFQEKMTD
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SGTNWLIEILCLIHSNGDPKWIQSVPIWERSPWVETEMGYKLLSEEEGPRLFSSHLPI
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/protein_id="AAA29620.1"
/db_xref="GI:160342"
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/gene="histidine rich protein B"
complement (828. .1589)
/gene="histidine rich protein B"
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/gene="histidine rich protein A"</pre>
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/gene="histidine rich protein B"
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l Similarity 95.8%;
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/gene="histidine rich protein D"
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'db_xref="G1:16209103"
'translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR
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Haldimann,A. and Wanner,B.L.
Direct Submission
Submitted (29-JUL-2001) Biological Sciences, Purdue University,
Lilly Hall, West Lafayette, IN 47907, USA
1.ccation/Qualifiers
1.-2959
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CRIM plasmid pAH120
artificial sequences; vectors.
1 (bases 1 to 2959)
1 Haldimann, A and Wanner, B.L.
Conditional replication, integration, excision, and retrieval plasmid-host systems for gene structure-function studies of
                      complement (2141. .2650)
/note="putative VECTOR sequence Bacteriophage lambda
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gone "histidine rich protein C"
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/gene="histidine rich protein C"
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complement(33..320)
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CRIM plasmid pAH120, complete sequence.
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/codon_start=1
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PVLFVKTDLSGALNELQDEAARLSWLATTGVPCAAVLDVVTEAGRDWLLLGEVPGQDL
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QDIALATRDIAEEEGWADPFLVLVQIAAPDSQRIAFYRLLDEFF"
718 c 758 t
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ANMDNFFAPVFTMGKYYTQGDKVLMPLA1QVHHAVCDGFHVGRMLNELQQYCDEWQGG
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and
lacz gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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                                                                                                                                93.3%; Score 22.4; DB 12; Length 2959;
95.8%; Pred. No. 28;
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
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Integration vector pCD11PKS
artificial sequences; vectors.
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VLERPPPRWSGNSPYSESYYARSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEE
ARTDRPSQQLRSLNGEWLTRPVAAH"
2972. .3081
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Integration vector pCD11PSK chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacZa) genes, complete cds.
AF178450
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Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Direct Submission
Submitted (18-8409) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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/note="attP; attachment site from bacteriophage lambda"
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1. 385

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0; Mismatches
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Pred. No. 27
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IPSTSRGGPVPNSPYSESYYARSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEE ARTDRPSQQLRSLNGEWLTRPVAAH"
2972. .3081
70628 multiple cloning site"
1 798 c 802 g 918 t
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COMPLEMENT (2423. .3217)
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Haldimann,A. and Wanner,B.L.
Direct Submission
Submitted (29-UUL-2001) Biological Sciences, Purdue University,
Lilly Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
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artificial sequences; vectors.
1 (bases I to 3663)
Haldimann, A. and Wanner, B.L.
Conditional-replication, integration, excision, and retrieval plasmid-host systems for gene structure-function studies of
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                                                                                                                     Length 3485;
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                                                                                                                    93.3%; Score 22.4; DB 12;
95.8%; Pred. No. 27;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                      CRIM plasmid pAH63, complete sequence.
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'db_xref="G1:16209152"
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ITKPFSPKELVARIKAVMRRISPMAVEEVIEMQGLSLDPTSHRVMAGEEPLEMGPTEF
KLLHFFWTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKALEPGGHDRNVQTV
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SSHLAPREKYSIMADAMRIHTLDPATCPPDIAGKRI ERRATRWEAGLVDQDDLDE
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Haldimann,A. and Wanner,B.L.
Direct Submission
Submitted (29-UUL-2001) Biological Sciences, Purdue University, Lilly Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
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Length 3663;
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    DB 12;
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21475783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 3695
/organism="CRIM plasmid pAH150"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (38. .193)
//note="araB7" terminal fragment"
198. .507
/note="araB3p"
                                                                                                                                                                                                                           3695 bp DNA
CRIM plasmid pAH150, complete sequence.
AY048733
Score 22.4; DI
Pred. No. 27;
0; Mismatches
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                                                                                                                             1783 GTTCAGCTTTTTTATACTAGTTG 1806
                                                                                                                                                                                                                                                                                                                                  CRIM plasmid pAH150
CRIM plasmid pAH150
artificial sequences; vectors.
1 (bases 1 to 3695)
Haldimann, A. and Wanner, B.L.
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                                                                                   1 GTTCAGCTTTTTGATACTAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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  93.3%;
95.8%;
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Thu Dec 4 08:47:33 2003

Db 18

Search completed: December 3, 2003, 13:18:42 Job time : 653.562 secs

5 22.4 93.3 473 13 BQ156404 6 22.4 93.3 597 12 B1422679 8 22.4 93.3 712 28 AQ991039 9 22.4 93.3 712 28 AQ990109 10 22.4 93.3 743 28 AQ990346 11 22.4 93.3 769 28 AQ990110 12 21.4 89.2 395 28 AQ991303 13 21.4 89.2 751 28 AQ99156	20.8 86.7 672 28 AQ990864 20.8 86.7 770 28 AQ990861 20.8 86.7 770 28 AQ991774 20.8 86.7 791 28 AQ991774 20.8 86.7 791 28 AQ991388 19.8 82.5 756 28 AQ991352 19.8 82.5 756 28 AQ991722 19.2 80.0 675 28 AQ91741	24 19.2 80.0 708 28 AQ990869 25 19.2 80.0 766 28 AQ990869 26 18.8 78.3 530 28 AZ26355 27 18.8 78.3 559 28 AZ300017 28 18.8 78.3 653 14 CB422481 29 18.8 78.3 676 29 AG147616 30 18.8 78.3 891 29 AG993964. 31 18.2 75.8 259 10 BG156704	33   18.2   75.8   388   13   BQ697293   BQ697293   NXPV   055     34   18.2   75.8   38.9   9   AW758311   BW7511   NXNV   094     35   18.2   75.8   403   9   AW153070   BW510914   BW510914   BW510914   BW510914   BW510914   BW510914   BW510914   BW510914     37   18.2   75.8   404   13   BU493456   BU493456   ND ADGR   DU493456   ND ADGR	ALIGNMENTS 64 bp DNA lir	Rfc01864 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01864, genomic sequence. AQ991011 AQ991011. GI:9649605 GSS. Photorhabdus luminescens Photorhabdus luminescens Photorhabdus luminescens Bacteria; Enterobact Bacteria; Enterobact Britarnharterianese.	REFERENCE I (bases 1 to 664) AUTHORS ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. TITLE A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000) REDLINB 20378633 PUBMED Conteat: ffrench-Constant RH Department of Biology and Biochemistry University of Bath South Bullding, Bath BA2 7AY, UK	Tel: (44) 1225 82651 Fax: (44) 1225 826779
GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: December 3, 2003, 12:13:45; Search time 1076.23 Seconds (without alignments)	ritle: Perfect score: 24 Sequence: 1 gttcagctttttgatactaagttg 24 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 22781392 seds, 12152238056 residues	otal number of hits satisfying chosen para inimum DB seq length: 0 aximum DB seq length: 2000000000 ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:*  1: em_estba:* 2: em_esthum:* 4: em_esthum:* 5: em_estru:* 6: em_estpl:* 7: em_estpl:* 8: em_htc:* 9: gb_est2:* 10: gb_est2:*		20: em_gss_vrt:* 21: em_gss_fun:* 22: em_gss_fun:* 23: em_gss_mus:* 24: em_gss_nvs:* 25: em_gss_rod:* 26: em_gss_rod:* 27: em_gss_vr1:* 28: gb_gss_l:* 29: gb_gss_l:*	the number than or the by anal	22.4 93.3 472 13 BQ157398 BQ157398 BQ157398

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Query Match
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BY115594
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Expressed Sequence Tage from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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/clone lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
                                                                                                                                                                                                                                                                                                                                                   /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus." 146 c 162 g 175 t 3 others
                   This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                       /dev stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 bp mRNA linear BST 24-
NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
NF092F02IR 5', mRNA sequence.
BQ156416
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0
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7391
                                                                                                                                                                                  /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="Mla".
/db xref="taxon:29488"
/clone="PLG01864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: gdmay@noble.org
Insert Length: 206 Std Error: 0.00
Plate: 092 row: F column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                         Location/Qualifiers
Email: bssrfc@bath.ac.uk
                                                                                                Seq primer: M13 Forward
Class: shotgun.
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EST.
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                                                                                   Acids Res.
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BQ156416/c
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KEYWORDS
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kuyosawa, Y., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Osato, N., Saito, R., Suzuki, H., Schonbach, C., Qoloboth, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schtriml, L.M., Kananaka, M. Matsuda, H., Batalov, S., Quackenbush, J., Bradt, D., Brusic, V., Chothia, C., Corbani, J. E., Cousins, S., Dallak, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gauteincich, S., Hirokawa, N., Jackson, I.J., King, B.L., Konagaya, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Magashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Randelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sullani, R., Schneider, C., Wang, Y., Watanabe, Y., Wang, I., Yang, Z., Zavolan, M., Yang, J., Makawa, T., Komo, H., Nakawa, T., Kanano, Y., Kananici, P., Hayateu, N., Hash, Laue, Y., Sakai, M., Yang, J., Yang, J., Watanki, Y., Sakai, K., Sakai, J., Sakai, Y., Sakai, Y., Sakai, J., Sakai, Y., Sakai, J., Birner, A., Sakai, Y., Sakai, J., Birner, A., Sakai, Y., Sakai, J., Birner, J., Bander, J., Sakai, Y., Sakai, J., Sakai, J., Wangaya, J., Birney, J., Wangaya, J., Birney, J., Sakai, S., Rasai, J., Sakai, S., Rasai, J., Sakai, S., Rasai, J., Sakai, S., Rasai, J., Sakai, S., Sakai, S.,
48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. CDNA was prepared from poly4+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The CDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XII-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVII5594 RIKEN full-length enriched, 18 days embryo whole body Mus musculus cDNA clone L430040C03 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
1 (bases 1 to 299)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 22.4; DB 13; Length 206; 95.8%; Pred. No. 37;
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Mus musculus
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/note="Vector: Landad Zap; Seedlings were exposed either
/note="Vector: Landad Zap; Seedlings were exposed either
damma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coll strain XLI-Blue MRF'
(Stratagene) Excised plasmids were plated using SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ156404 173 bp mRNA linear EST 24.APR-2002 NF092E03IR1F1023 Irradiated Medicago truncatula cDNA clone
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spernatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids
; eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7380
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 473 Std Brror: 0.00
Plate: 092 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
        USA
2510 Sam Noble Parkway, Ardmore, OK 73402, USJ Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 472 Std Error: 0.00
Plate: 104 row: D column: 07
Seg primer: TCACACAGABAACAGCTATGAC.
                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF104D071R"
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1 Similarity 95.8%; Pred. No. 48;
23; Conservative 0; Mismatches
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BQ156404.1 GI:20293463
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Matches 23; Conserv
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraises for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken propers mouse figures.
                          Email: genome_res@gsc.riken.go.jp,
URL:http://genome_gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,Aizawa,K., Akimura,T., Inch,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sahazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
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/dev_stage="18 days embryo"
/clone_lib="RIKEN full-length enriched, 18 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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NPI04D07IR1F1062 Irradiated Medicago truncatula cDNA clone
NPI04D07IR 5', mRNA sequence.
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Plant Biology Division
The Samuel Roberts Noble Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L430040C03"
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South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG01894"
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l Similarity 95.8%;
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Best Local Similarity 95.8%;
Matches 23; Conservative
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                                                                                                                      /drs stage="seedlings"
/done_lib="Irradiated"
/clone_lib="Irradiated"
/clone_lib="Vertor: Lambda 220; Seedlings were exposed either
/clone_lib="Vertor: Lambda 220; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Giagack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using Exassist
helper phage and the E. coll strain XLI-Blue MRF.
(Stratagene). Excised plasmids were plated using SOLR
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; endicotyledons; core eudicots;
asterids; laminds; Solanales; Solanaceae; Solanum; Lycopersicon.

[ (bases 1 to 597)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Ling,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,J.C.M., Praser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue
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TAMU Lycopersicon esculentum cDNA clone
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/dev stage="25-40 days old"
/lab_host="XL1-Blue MRF",
/lab_host="XL1-Blue MRF",
/loone_lib="tomato callus, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Glovannoni laboratory; ciEc - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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                    organism="Medicago truncatula"
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Pred. No. 48
                                                                                                           /tissue_type="seedlings"
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ESTE33345 tomato callus, TAMU Ly
CLE711G2 5' end, mRNA sequence.
BI422679
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clone="clEC71G2"
                                       /mol_type="mRNA"
/db xref="taxon:3880"
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                                                                                   clone="NF092E03IR"
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/cultivar="TA496"
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95.8<del>8</del>;
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Best Local Similarity
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148 c 165 g 187 t 2 others
Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae; Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01894, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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                                                                                                                                 Score 22.4; DB 12; Length Pred. No. 51; 0; Mismatches 1; Indels
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Pred. No. 54;
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Department of Biology and Biochemistry
University of Bath
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                            Contact: ffrench-Constant RH
Department of Biology and Biochemistry
Department of Biology and Biochemistry
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South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Fax: (44) 1225 826779
Fax: (51) F
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Department of Biology and Biochemistry
Department of Biology and Biochemistry
Department of Biology and Biochemistry
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Fax: (44) 1225 xendom reads from the M13 library. For This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Rfc00827 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00827, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/organism="Photorhabdus luminescens"
/mol type="genomic DNA"
/strain="W14"
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95.8%; Pred. No. 55;
ive 0; Mismatches
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/clone="PLG01106"
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Class: shotgun.
Location/Qualifiers
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AQ990110.1 GI:9648704
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Best Local Similarity 95.8
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bastc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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Enterobacteriaceae; Photorhabdus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                             AQ990809
Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01638, genomic survey
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Rfc01106 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
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1 (bases 1 to 743)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/mol_type="genomic DNA"
/strain="W14"
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Department of Biology and Biochemistry
University of Bath
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/clone="PLG01638"
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Class: shotgun.
Location/Qualifiers
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Photorhabdus luminescens
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AQ990809.1 GI:9649403
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GSS 14-AUG-2000
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I (bases 1 to 39.)

Ifrench-Constant, R. H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

Agenomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: ffrench-Constant RH
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Fax: (44) 1225 826779
Fax: (54) 1225 826779
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
                                                                                                                                                                                                                                                                                              AQ991303
Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
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                                                             Length 769;
                                                                                                       Indels
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                                                           Score 22.4; DE
Pred. No. 55;
0; Mismatches
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/strain="W14"
/db_xref="taxon:29488"
/clone="PLG02205"
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ilarity 91.7%;
Conservative C
                                                             93.3%;
95.8%;
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                                                           Query Match
Best Local Similarity 95.8
Matches 23; Conservative
163
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223 a
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Best Local Simi
Matches 22;
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AQ989566/c
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AQ991303/c
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Enterobacteriaceae; Photorhabdus.

I (bases 1 to 7.6)

Ifranch-Constant, R. H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P. J., Bowen, D. and Blattner, F.R.

Agenomic Sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
library"
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/clone_lib="Photorhabdus luminescens strain W14 M13
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93.3%; Score 22.4; DB 28; Length 764;
Best Local Similarity 95.8%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 1; Indels 0

    764
/organism="Photorhabdus luminescens"

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Department of Biology and Biochemistry
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Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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/strain="W14"
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/clone="PLG01245"
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/clone="PLG00827"
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                 Seg primer: M13 Forward Class: shotgun.
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AQ990470/c
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ACCESSION VERSION KEYWORDS

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REFERENCE AUTHORS

TITLE

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DEFINITION

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS MEDLINE PUBMED

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TITLE

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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
146 c 161 g 179 t 2 others
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                         Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli X12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
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Enterobacteriaceae; Photorhabdus.
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Rfc01698 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01698, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
library"
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     Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20378633
10919786
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1. .672
/organism="Photorhabdus luminescens"
                                                                                Contact: ffrench-Constant RH
Department of Biology and Biochemistry
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Department of Biology and Biochemistry
University of Bath
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/strain="W14"
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/clone="PLG01701"
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
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Photorhabdus luminescens
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Class: shotgun.
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AQ990861/c
LOCUS
DEFINITION
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ffrench-Constant, R.H., Materfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic Sample sequence of the entomopathogenic bacterium
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Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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159 c 171 g 200 t 4 others
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                                                                                                                                                                                 Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus
Rfc00126 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00126, genomic survey
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Rfc01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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Department of Biology and Biochemistry
University of Bath
                                                                                                                                                                                                                                      Enterobacteriaceae; Photorhabdus
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/strain="W14"
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Class: shotgun.
Location/Qualifiers
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AQ990864/c LOCUS DEFINITION

RESULT 14

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BASE COUNT ORIGIN

FEATURES

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

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Class: shotgun.

Location/Qualifiers

1. 752

Lorganism="Photorhabdus luminescens"

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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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86.7%; Score 20.8; DB 28; Length 753;

Best Local Similarity 91.7%; Pred. No. 2.6e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0;
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Search completed: December 3, 2003, 14:49:19 Job time : 1079.23 secs

638 GTTCAGCTTTTTATACTAAGTGG 615

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December 3, 2003, 12:13:45; Search time 652.562 Seconds (without alignments) 1504.579 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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24
1 caacttagtatcaaaaagctgaac 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM nucleic - nucleic search, using sw model
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Query Match Length DB	.0 243		.3 201		.3 243	.3 361	610	.3 2758	.3 2959 1	.3 3485 1	3 3683 1	3698 8.	.3 4105 1	.3 4190 L	.3 4549 1	.3 4782 1	.3 5641	.3 5706 1	.3 5739 1	3 5771 1	.3 5814 1	.3 5826 6	.3 5911 1	.3 5986 1	.3 6000 1	.3 6043	.3 6200 1	.3 6664 1	.3 6668 1	3 7176 1	.3 39732 7	.3 42529 1	.3 42530 1	04 1	.3 48502 7				16 ce 5 from Patent	5	ייי פרייד פריים מייים פריים	tic construct	ial sequence	ъ.	e-specific WO 0116345	Peter (DE)
Score Ma	24 1	4. 6.	22.4	20.00	22.4	22.4	22.4	22.4	22.4	22.4	4. 4.	22.4.	22.4	22. 4. c.	22.2.4.	22.4	22.4	22.4	22.4	4. 6.	22.4	22.4	22.5	22.4.4	22.4	22. 22. 4. 4.	4. 4.	22.4	4. 6	22.4	22.4	22.4	4.00	22.4	22.4		·		AX092116			syntheti NISM syntheti			E Sequence NAL Patent:	
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PAT 26-JUL-1995
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Okano, K. and Kambara, H.
Okano, K. and Kambara, H.
Separation of polynucleotides using supports having a plurality of electrode-containing cells
Patent: US 5434049-A 18 18-JUL-1995;
Location/Qualifiers
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1 (bases 1 to 201)

1 (bases 1 to 201)

Okano, K. and Kambara, H.

Device for separating polymucleotides having a plurality of electrode-containing cells and movable collecting capillary Patent: US 5607646-A 18 04-MAR-1997;

Location/Qualifiers
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             /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32330"
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Sequence 18 from patent US 5434049.
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I13139.1 GI:910488
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93.3%; Score 22.4; E
Best Local Similarity 95.8%; Pred. No. 42;
Matches 23; Conservative 0; Mismatches
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93.3%; Score 22.4; Dest Local Similarity 95.8%; Pred. No. 42;
Matches 23; Conservative 0; Mismatches
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Sequence 18 from patent US 5607646.
136498.1 GI:2086323
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/organism="unknown"
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Matches 23; Conservative (
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Okano, K. and Kambara, H.
Polymucleotide capturing support for capturing, eluting and collecting polymucleotides in a sample solution
Patent: US 5817506-A 18 06-OCT-1998;
Location/Qualifiers
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                                                                                                                        ch 100.0%; Score 24; DB 6; Length 243; 1 Similarity 100.0%; Pred. No. 8.5; 24; Conservative 0; Mismatches 0; Indels
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/oxganiem="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texcn:32630"
/note="Oligonukleotid"
i a 34 c 34 g 101 t
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artificial sequences.
1 (bases 1 to 201)
Okano, K. and Kanbara, H.
CHIP FOR CATCHING POLYNUCLEOTIDE
Patent: JP 1993236997-A 11 17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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Artificial sequence, Genes.
Dr 1992328997-A/11
17-SEP-1993
28-FEB-1992 JP 1992042829
CKANO KAZUNOBU, KANBARA HIDEKI
                                                                                                                                                                                                                                                                                 201 bp Sequence 18 from patent US 5817506.
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38 c 27 g
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E05439.1 GI:2173628
JP 1993236997-A/11.
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PAT 10-APR-2001

AX092113/c LOCUS DEFINITION ACCESSION VERSION

RESULT 6

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ORGANISM

KEYWORDS

REFERENCE AUTHORS

JOURNAL

PEATURES

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/protein_id="BAA12823.1"
/db_xref="G1:1345406"
/translation="MSDDFIWFEGIAFPNMGFRSETLRKVRDEFVIKDEDVIILTYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MACHSS 1668 bp mRNA linear PRI 06-FEB-1999
Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxysteroid sulfotransferase subunit.
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis (crab-eating macaque)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 1668)
Ogura, K., Satsukawa M., Kato, K., Okuda, H. and Watabe, T.
Unpublished
2 (bases 1 to 1668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Pharmacy and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (B-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 610;
                      linear
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/organism="Macaca fascicularis"
/mol_type="mRn8"
/db_xref="texon:9541"
/clone="monHST-1"
                      DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%; Score 22.4; D
95.8%; Pred. No. 35;
iive 0; Mismatches
                                                                                                                                                                                                                                                    Targeted gene removal
Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
Location/Qualifiers
                                                                                                                   Nicotiana tabacum (common tobacco)
Nicotiana tabacum
                Sequence 1 from Patent WO0121780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="liver"
/clone_lib="lambda_gt11"
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                                                                              AX101000.1 GI:13619857
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D85521.1 GI:1345405
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Matches 23; Conservative
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Bacteriophage lambda
Bacteriophage lambda
Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.

L (bases 1 to 31)
Schmelsener,U., McKenney,K., Rosenberg,M. and Court,D.
Removal of a terminator structure by RNA processing regulates int
                                                                                                                                                                                               Bacteriophage lambda
Bacteriophage lambda
Viruses; deDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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                                                                                                                                                                                                                                                                                                              Sequence-specific dna recombination in eukaryotic cells
Patent: WO 0116345-A 2 08-MAR-2001;
Droege, Peter (DE)
Location/Qualifiers
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Location/Qualifiers
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/db_xref="taxon:10710"
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    243 /organism="Bacteriophage lambda"
/mol_type="genomic DNA"
/db_xref="taxon:10710"

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Best Local Similarity 95.8%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches
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                                                                                            Sequence 2 from Patent WOOll6345.
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  63 CAACTTAGTATAAAAAGCTGAAC 40
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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/transl_table=
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AY048723/C
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MITO28.1 GI:160339

MITO28.2 Mistidine-rich protein.

Plasmodium falciparum (malaria parasite P. falciparum)

Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 2758)

Lenstra,R., d'Auriol,L., Andrieu,B., Le Bras,J. and Galibert,F.

Cloning and sequencing of Plasmodium falciparum DNA fragments

Containing repetitive regions potentially coding for histidine-rich

proteins: identification of two overlapping reading frames

Blochem. Blophys. Res. Commun. 146 (1), 368-377 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="histidine rich protein A"
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DDQDYCTCTRRTIYEESMDNTVEFAKKMYELGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MYLFIYIFFFFFFFFFFVIVQKDIEQLDIKCAHEQMNIQKQYDE
KKKPLFEKRDEIIQKIPGFWANTLRKHPALSDIVPEDIDILNHLVKLDLKDNMDNNGS
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SFQSMKENKMSNFSLLSVDFVEEKAQLLRKGISGDWRNHLTVAQAEAFDKLFQEKMTD
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   SGTNWLIEILCLIHSNGDPKWIQSVPIWERSPWVETEMGYKLLSEEËGPRLFSSHLPI
                                                                                                                                                                              Gaps
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Location/Qualifiers
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protein_id="AAA29620.1"
/db_xref="G1:160342"
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P.falciparum histidine-rich protein genes.
M17028
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/gene="histidine rich protein B"
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/gene="histidine rich protein E"
complement (828. .1589)
/gene="histidine rich protein E"
                                                                                                                                            Score 22.4; DB 9;
Pred. No. 30;
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329 C
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2525...278 purcein C"
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/ gene="histidine rich protein D"
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/ gene="histidine rich protein D"
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Haldiann, A. and Wanner, B.L.
Direct Submission
Submitted (29-JUL-2001) Biological Sciences, Purdue University,
Lilly Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
1. - 2959
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1 (bases 1 to 2959)
Haldimann, A. and Wanner, B.L. Conditional-replication, integration, excision, and retrieval plasmid-host systems for gene structure-function studies of
complement(2141. .2650)
Totte="putative VECTOR sequence Bacteriophage lambda
(702459); putative"
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bb_xref="taxon:172348"
complement(33.,320)
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21475783
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95.8%; Pred. No. 28;
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Integration vector pCD11PSK
artificial sequences, vectors.
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1 Similarity 95.8%;
23; Conservative (
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                                                                                                                                                                                                                                                                                                                        AFI78449 3485 bp DNA linear SYN 20-JUL-2000 Integration vector pCD11PKS chloramphenicol transacetylase (cat) and beta-galactosidase alpha peptide (lacZa) genes, complete cds. AF178449
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LESHLAAPERTSVSIMADAMRIHTUDPARTOFPDHQAGRIR TEARTRWBAGLVDQDDLDE
EHQGLAPABLFARLKRAMPGGEDLVVTHGDACLPNINVENGRFSGFTDGGRLGVADRY
QDIALATRDIAEELGGEWADRFLVYTGIAAPDSQRIAFYRLLDEFF"
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2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
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Integration vector pCD11PKS
artificial sequences; vectors.
1 (Dases 1 to 3482)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/lab host="Escherichia coli"
1. .385
                                                                                                                               Score 22.4; DB 12;
Pred. No. 28;
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1 Similarity 95.8%;
23; Conservative (
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VLERPPPRWSSNSPYSESYYARSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEE ARTDRPSQQLRSLNGEWLTRPVAAH"
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ANMDNFPAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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Integration vector pCD11PSK chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacza) genes, complete cds.
AF178450
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Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
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/note="attP; attachment site from bacteriophage lambda"
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protein id="AAF86673.1"
db_xref="GI:9294790"
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1. .385
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Pred. No. 27;
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Length 3663;

circular SYN 17-OCT-2001

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/db_xref="G1:16209151"
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ITKPFSPKELVARIKAVMRRISPMAVEEVIEMQGLSLDPTSHRVMAGEEPLEMGPTEF
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Haldiamn, A. and Wanner, B.L.
Direct Submission
Submitted (29-JUL-2001) Biological Sciences, Purdue University,
Lily Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             CRIM plasmid pAH150
artificial sequences; vectors.

1 (bases I and 3891)
Haldimann, A. and 3891.
Conditional-replication, integration, excision, and retrieval plasmid-host systems for gene structure-function studies of
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                                                 DB 12;
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21475783
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/organism="CRIM plasmid pAH150"
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complement(38. .193)
/note="araC' terminal fragment"
                                                                                                                                                                                                                                                 CRIM plasmid pAH150, complete sequence. AY048733
                                                                                  0; Mismatches
                                                   Score 22.4;
Pred. No. 27;
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IPSTSRGGPVPNSPYSESYYARSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEE ARTDRPSQQLRSLNGEWLTRPVAAH"
2972. :3081
2972. :3081
708 c 902 g 918 t
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db_xref="d1:16209076"

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ADGSGTSFVFTSYLAKYNEEWRQNVGTGSTVKWPIGLGGKGNDGIAAFPRORLPGAIGY
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BHQGLAPABLFARLKRAMPDGBDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY
QDIALATRDIABELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
complement (3174. .3663)
                                                                                                                                                                                                                                                                                                                                               circular SYN 17-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 3663)
Haldiann,A. and Wanner,B.L.
Direct Submissor.
Submitted (29-UU-2001) Biological Sciences, Purdue University,
Lilly Hall, West Lafayette, IN 47907, USA
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                                                                                                                                       Length 3485;
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                                                                                                                                   93.3%; Score 22.4; DB 12; 95.8%; Pred. No. 27;
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1475783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="CRIM plasmid pAH63"
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/db_xref="taxon:172341"
101. 1030
                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                       CRIM plasmid pAH63, complete sequence.
AY048716
                                                                                                                                                       Pred. No. 27;
0; Mismatches
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892 c 914 g 903 t
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/db_xref="GI:16209077"
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                                                                                                                                                                                                                                             834 chactragrarahahahaccreahc 811
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CRIM plasmid pAH63
artificial sequences, vectors.
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/transl_table=11
/product="Psts"
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producī="kan"
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/gene="pstS"
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                                     misc_feature
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ORIGIN
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AUTHORS
TITLE
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1838 CAACTTAGTATAAAAAGCTGAAC 1815

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Search completed: December 3, 2003, 13:18:43 Job time : 653.562 secs

203, App 69, Appl 69, Appl 69, Appl 69, Appl 11, Appli 1

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US-08-021-667A-18/c
; Sequence 18, Application US/08021667A
; Parent NO. $434049
; Parent NO. $434049
; Parent NO. $434049
; Parent NO. $434049
; Parent NO. $434040
; Parent NO. $434040
; PAPLICANT: Okano, Kazunori
; APPLICANT: Kambara, Hideki
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND TITLE OF INVENTION: METHOD USING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
; STREET: Suite 600, 1919 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
                                                                                                                                                                                                                                                                                                Sequence Sequence Sequence Sequence Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSAIT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 520.31930X00
TELEPAX: 202-828-0300
TELEPAX: 202-828-0300
TELEPAX: 202-828-0300
TELEPAX: 202-828-0300
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TELEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 basis single
TYPE: nucleic acid
STRANDEDNES: single
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95.8%; Pred. No. 0.28;
iive 0; Mismatches 1;
US-09-312-283C-28
US-09-312-283C-203
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US-08-482-273-69
US-08-342-268-69
US-09-012-968-69
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US-09-068-101-10
US-09-068-101-10
US-09-233-493-11
US-09-233-493-11
US-09-205-476-13
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HYPOTHETICAL: YES
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    linear
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Matches 23; Conserv
    US-08-021-667A-18
                                                                                                                                          December 3, 2003, 12:13:45; Search time 28:562 Seconds (without alignments) 370.884 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 41, Ar
Sequence 667, A
Sequence 28, Ar
Sequence 203, A
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Sequence 5, Al
Sequence 5, Al
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-126-18

US-08-556-978B-78

US-09-296-280-43

US-09-296-280-43

US-09-296-280-42

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US-09-296-280-15

US-09-296-280-5

US-09-296-280-5

US-09-296-280-5

US-09-296-280-5

US-09-296-280-5

US-09-296-280-1

US-09-296-280-3

US-09-296-280-3
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                                                                                                                                                                                                                                                                                1 caacttagtatcaaaaagctgaac 24
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                                                                                              OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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24
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Match Length
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Perfect score:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Patent No. 5607646

GENERAL INFORMATION:

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CONTINUED OF INVENTION:

CONTROLED OF INVENTION:

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NVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
NVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
NVENTION: METHOD USING SAME
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Pred. No. 0.28;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520.31930X00
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US-08-728-785A-18/c
) Sequence 18, Application US/08728785A
; Patent No. S817506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/021,667
FILLING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
TELEFAX: 202-828-0380
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SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 95.8
Matches 23; Conservative
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MEDIUM TYPE: Floppy
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APPLICANT: Okano, Ka:
APPLICANT: Kambara, ITILE OF INVENTION:
ITILE OF INVENTION:
ITILE OF INVENTION:
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ZIP: 20006
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Length 201;
CORRESPRONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREST: Suite 1800, 1300 No. 5817506th Seventeenth St.
CITY: Arington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Patent No. 6268169
GENERAL INFORMATION:
JAPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINTON
STATE: DELAMARE
CONNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILING APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,544
FILING DATE: 1.-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-PRE-1993
ATTORNEY/AGENT INFORMATION:
NAME: TEXTY, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.3%; Score 22.4; DB 1;
95.8%; Pred. No. 0.28;
tive 0; Mismatches 1;
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COMPUTER READABLE FORM:
MEDIUM TYPES DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520.31930X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAACTTAGTATCAAAAAGCTGAAC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Terry, David T. REGISTRATION NUMBER:
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Sequence 43, Application US/09296280

Patent No. 6277608

GENERAL INFORMATION

APPLICANT: Hartley, James L.

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Prox, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REPREBUCE: 0942.285007

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT APPLICATION NUMBER: US/0177,387

EARLIER APPLICATION NUMBER: US/0177,387

EARLIER PILING DATE: 1999-10-23

FARLIER PILING DATE: 1997-10-24

NUMBER: PatentIN Ver: 2.0

SOFTWARE: PatentIN Ver: 2.0

SEQ ID NO 43

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/09296280

Sequence 42, Application US/09296280

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTHARE: Patentin Ver. 2.0
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Unknown
FEATURE:
CHER INFORMATION: Description of Unknown Organism: recombination
COTHER INFORMATION: products
US-09-296-280-43
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                                               Query Match

93.3%; Score 22.4; DB 1; Length 7652;
Best Local Similarity 95.8%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.3%; Score 21.2; DB 3; Length 25; Best Local Similarity 83.3%; Pred. No. 0.87; Matches 20; Conservative 3; Mismatches 1; Indels
                                                                                                      0; Mismatches
                                                                                                                                                                                                     6094 CAACTTAGTATAAAAAGCTGAAC 6071
                                                                                                                                                      1 CAACTIAGIATCAAAAAGCTGAAC 24
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US-07-590-988A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTAL:

ZIF: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Disfette - 3.50 inch, 800Kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh OF SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,988A FILING DATE: 19901001
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
MAME: Nicholas J. Seay
REFERENCE/DOCKET NUMBER: 27,386
FREFERENCE/DOCKET NUMBER: 27,386
FREFERENCE/DOCKET NUMBER: 27,386
FREFERENCE/DOCKET NUMBER: 3629691682
FELECOMMUNICATION INFORMATION:
TELLEPHONE: (608) 251-5000
TELLEPAN: (608) 251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
'PMGTH: 7652 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-590-988A-1/c
; Sequence 1, Application US/0759098A
; Patent No. 5527288
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
    ADDRESSED Quarles and Brady
    STREET: P.O BOX 2113
    STREET: P.O BOX 2113
    STREET: PIRST WISCONSIN PLAZA
    COUNTRY: U.S.A.
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DESCRIPTION: synthetic recombinant plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2355 CAACTTAGTATAAAAAGCTGAAC 2378
                                                                                                                                                                                                   CR-9389-A
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                                                                 08/077,600
                               PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/077,60.
FILING DATE: UNB 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9;
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 4909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 7652 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 95.8
                                                                                                                                                                                                                                                               302-773-0164
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Matches
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-09-655-728-7/c
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                                                                                                                                                                                                                                       Gape
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OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-296-280-42
                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: CAMERON, Beatrice
APPLICANT: WILS, Pierre
APPLICANT: MIS, Pierre
APPLICANT: MANGEOUPES, PREPARATION THEREOF AND TITLE OF INVENTION: USE THEREOF IN GENE THEREOF AND
                                                                                                                                                               Length 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,511
FILING DATE:
CLASSIFICATION 1514
FRIDK APPLICATION DATA:
APPLICATION NUMBER: BS 95/02117
FILING DATE: 23-FEB-1995
FRIDK APPLICATION DATA:
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-196
ATOMNEY/AGENT INFORMATION:
APPLICATION NUMBER: 29,699
FREISTRATION NUMBER: 3908
FILING APPLICATION NUMBER: ST95013-US
FREISTRATION NUMBER: 3908
FREISTRATION NUMBER: ST95013-US
FREISTRATI
                                                                                                                                                   ch 85.0%; Score 20.4; DB 3; 1 Similarity 75.0%; Pred. No. 1.9; 18; Conservative 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.8%; Score 19.4; DB 3; 95.2%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Rhone-Poulenc Rorer Inc.
1: 500 Arcola Road, Mailstop 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                    1 CAACTTAGTATCAAAAAGCTGAAC 24
                                                                                                                                                                                                                                                                                                                                         |:|:||:|||
24 CMASTIWGTAYAARAAGCIGAAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08894511
Patent No. 6143530
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.2°
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poul
                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-894-511-7
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1 CAACTTAGTATCAAAAAGCTG 21

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                                                                                                                          WILS, Pierre
DARGUET, Anne-Marie
DARGUET, Anne-MoleCULES, PREPARATION THEREOF AND
USE THEREOF IN GENE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning Using Engineered
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPER FICHORY:

MEDIUM TYPER FICHORY:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,728

FILING DATE: 05-Sep-2000

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/894,511

FILING DATE: CUNKNOWN>

RPLICATION NUMBER: 08/894,511

FILING DATE: 21-FEB-196

ATTORNEY/ART INFORMATION:

NAME: Savitzky Beq., Martin F.

REGISTRATION NUMBER: 29,699

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: 29,699

REFERENCE/DOCKET NUMBER: ST95013-US

TELECOMMUNICATION INDORMATION:

TELEBHONE: (610) 464-3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: /desc = "Oligonucleotide' SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.8%; Score 19.4; 95.2%; Pred. No. 5.
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Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational
; TITLE OF INVENTION: Recombination S
; NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAACTTAGTATCAAAAAGCTG 21
Sequence 7, Application US/09655728
Patent No. 6492164
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
SCHERMAN, Daniel
CAMERON, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 CAACTTAGTATAAAAAGCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.2%
                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-233-493-15/c
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us-10-082-772-4.rni

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Gaps
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US-09-233-492-15/c
; Sequence 15, Application US/09233492
; Patent No. 6270969
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; TITLE OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: No New York Ave., N. W. Suite 600
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.2; 'DB 3; Length 25; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                 FILING DALE,
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEPHONE: 202-371-2540
SQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 15:
SQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 15:
SQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 15:
SQUENCE ACCURATE SEQ ID NO: 15:
TYPE: NUCleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAACTTAGTATCAAAAAGCTGAAC 24
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
FILING DATE: 07-JUN-1995
CLASSIFICATION:
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TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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Patent No. 6171861

CENERAL INFORMATION

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

STRTE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                CITY: Washington
CITY: Washington
CITY: Washington
COUNTRY: USA
ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 12-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 00-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 06/486,139
FILING DATE: 07-JUN-1995
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ZIP: 2005-3934
COMPUTER READBLE FORM:
MEDIUW TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: PATORILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAACTTAGTATCAAAAAGCTGAAC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
MOLECULE TYPE: Cl
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US-09-005-476-15/c
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Length 25;

DB 3;

80.0%; Score 19.2;

Query Match

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APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
CORRESPONDENCE: 31
CORRESPONDENCE: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ښ</u>
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07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application PC/TUS9610082A GENERAL INFORMATION:
                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIPTCATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECHOMUNICATION INPORMATION:
TELECHOMONICATION INPORMATION:
TELECHOMONICATION:
TELECHOM
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CLASSIFICATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPANS: 202-371-2600
IELEPANATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
TWATH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.5%;
Matches 21; Conservative
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STRANDEDNESS: both
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20005-3934
                                               FILING DATE: 1
CLASSIFICATION:
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PCT-US96-10082A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-498-074-15
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                                                                                                                                                                                                                                                                                                                                                                           FALENT NO. SLIGHER
FALENT NEORAMION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Tengle, Gary F.
FULL CANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.285007
CURRENT APPLICATION NUMBER: US 09/296,280
CURRENT APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1999-10-23
EARLIER FILING DATE: 199-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PALENT NOS: 60
                                               Gaps
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US-09-296-280-15
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERRE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 19.2; DB 3; Length 25; 87.5%; Pred. No. 6.5;
                                           3; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
Best Local Similarity 87.5%; Pred. No. 6.5; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                         24 CAACTTTGTACAAAAAGCTGAAC 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09296280 Patent No. 6277608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-498-074-15/c
; Sequence 15, Application US/09498074
; Patent No. 6534264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.5'
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Herewith)
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                            RESULT 13
US-09-296-280-15/c
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STATE:
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Gaps

; 0 0; Gaps Best Local Similarity 87.5%; Pred. No. 6.5; Matches 21; Conservative 0; Mismatches 3; Indels

1 CAACTTAGTATCAAAAAGCTGAAC 24

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Search completed: December 3, 2003, 14:51:47 Job time: 29.562 secs

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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AQ991039 REC01634
AQ990346 REC01638
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AQ990340 REC01645
AQ9903103 REC01265
AQ9903103 REC01265
AQ990368 REC01268
AQ990368 REC01268
AQ990388 REC01153
AQ99173 REC01638
AQ99173 REC01638
AQ99173 REC0113
AQ99135 REC0113
AQ99135 REC0113
AQ99135 REC01706
AQ99135 REC01706
AQ99137 REC01689
AZ26325 RPCI -23-1
CB42241 REC0132
AQ99137 REC0196
AZ26325 RPCI -23-1
CB42241 REC0132
AQ99137 REC0196
AZ26325 RPCI -23-1
CB42241 REC0132
AQ99133 REC0196
AZ26329 RPCI -23-3
AG991307 RES10914
AUS1070 RE34206
BG156704 RBS10914
AUS1073 MP93912.X
AZ41383 LOCUS AG256781 LOCUS AG256781 LOCUS AG256781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photorhabdus luminescens
Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.

1 (bases 1 to 664)
1 (french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Pappl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ991011
Rfc01864 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01864, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Ballding, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                           AQ991039
AQ990809
AQ990346
AQ990110
AQ990470
AQ991303
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AQ990869
AQ990173
AZ263252
AZ300017
AG147616
AQ9757016
AG093904
BG156704
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BY510914
AW153070
BU493456
BG317764
AI449436
AI510342
AZ413832
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AQ991011.1 GI:9649605
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BQ156416 NF092F021
BY115594 BY115594
BQ157398 NF104D071
                                                                                                                                   3, 2003, 12:13:45; Search time 1076.23 Seconds (without alignments) 541.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                              22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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93.3
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GSS 14-AUG-2000

Score

Result No.

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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
; eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 24-APR-2002
                                                                                                                                                                                                                                                                                                                                                                           /note="Genomic DNA from strain W14 was size selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="seedlings"
/dev stage="seedling"
/clone_lib="!tradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8%; Score 23; DB 28; Length 664; 95.8%; Pred. No. 30; 1: Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               3 others
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Email: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                    kb) and then cloned into M13 Janus."
                                                                                                                                                                                                   organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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Unpublished
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Insert Length: 206 Std Error: 0.00
Plate: 092 row: F column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG01864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 CAACTTAGTATNAAAAAGCTGAAC 638
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                                                                                                          Seg primer: M13 Forward
Class: shotgun.
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BUKARYOTA METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. BUKARYOTA; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. CKazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schonbach, C.; Ouachos, J.; Shrimi, L.M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Bais, C.; Corbani, L.B.; Cousins, S.; Dalla, B.; Darusic, V.; Chothia, C.; Corbani, L.B.; Cousins, S.; Dalla, B.; Dradt, D.; Brusic, V.; Chothia, C.; Corbani, L.B.; Kanai, A.; Kawai, H.; Kawasawa, Y.; Kedzierski, R.M.; Jarvis, B.D.; Kanai, A.; Kawai, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.; Kuschkin, I.V.; Lee, Y.; Lenhard, B.; Lyons, P.A.; Maglott, D.R.; Marchhonni, I.; McKenzie, L.; Minia, P. P. Ramachandran, S.; Randsi, T.; Marchhonni, I.; McKenzie, L.; Miniada, K.; Sandelin, A.; Schneider, C.; Semple, C.A.; Setou, M.; Shimada, K.; Sullana, R.; Taylor, M.; Shimada, K.; Sullana, R.; Taylor, M.; Taylor, M.; Shimada, K.; Sullana, R.; Taylor, M.; Sandelin, A.; Savolan, Y.; Rama, J.; A.; Yanagisawa, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Azawa, K.; Azawa, T.; Komo, H.; Marane, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Azawa, K.; Shinagawa, A.; Hashizume, M.; Materston, R.; Shinagawa, A.; Bara, A.; Hashizume, M.; Materston, R.; Shinagawa, M.; Matanishi, A.; Matanishi, M.; Matanishi, M.; Matanishi, M.; Matanishi, M
48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. CDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The CDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing CDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
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Pred. No. 37;
0; Mismatches
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BY115594.1 GI:26226695
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1 Similarity 95.8%;
23; Conservative
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Matches 23
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Score 22.4; 1
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95.8%;
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                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
JR.inttp://genome.gsc.riken.go.jp,
Alizawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Akimura.T., Toth,M., Kawai,J., Konno,H., Miyazaki,A., T., Imotani,K., Ishii,Y., Itoth,M., Rawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ157398 A72 bp mRNA linear BST 24-APR-2002 NF104D07IR1F1062 Irradiated Medicago truncatula cDNA clone NF104D07IR 5', mRNA sequence.
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledone; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae, Trifolieae;
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/clone_lib="RIKEN full-length enriched, 18 days embryo
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/mol type="mxNa"
/strain="C5731/67"
/db_xref="taxon:10090"
/clone="L43004003"
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Plant Biology Division
The Samuel Roberts Noble Foundation
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BQ156404 1inear EST 24-APR-2002 NF092E03IRIF1023 Irradiated Medicago truncatula cDNA clone NF092E03IR 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
eurosids I; Fabales; Fabaceae, Papilionoideae, Trifolieae;
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Plant Biology Division
The Samuel Roberts Noble Foundation
250 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7390
Email: gdmay@noble.org
Insert Length: 473 Std Error: 0.00
Plate: 092 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.
2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391
Eax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 472 Std Error: 0.00
Plate: 104 row: D column: 07
Seq primer: TCAAAGABAAAGCTATGAC.
Location/Qualifiers
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/mol type="genomic DNA"
/stzin="W14"
/db_xref="taxon:29488"
/clone="PLG01894"
                                                                                                                                                                                                                                                                                                                                                695 bp
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Photorhabdus luminescens
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Class: shotgun.
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Best Local Similarity 95.8%;
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                                                                                         /tissue_type="seedlings"
/dev_stage="seedlings"
/dev_stage="seedlings"
/clone_lib="irradiated"
/note="Vector: Lambda_Zap; Seedlings were exposed either
/note="Vector: Lambda_Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
polyk+ enriched, pooled sample of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap Xx vector (Stratagene) and
packaged using the digapack III Gold packaging extracts.
Phagemids containing-CDNA inserts were in vivo excised
from the recombinant Uni-Zap Xx vector using ExAssist
helper phage and the E. coli strain XLI-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 597)

Alcala,J., Virbalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning C.M., Fraser,C.M., Matrin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue
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/tissue_type="25-40 days old"
/dev_stage="25-40 days old"
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/lone_lib="tomato callus, TAMU"
/note="Wortor: pBlueScript SK(-); Site_1: BcoRl; Site_2:
Xhol; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
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SST533345 tomato callus, TAMU Lycopersicon esculentum cDNA clone CLEC71G2 5' end, mRNA sequence.
BI422679
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22.4; DB 13; Length 473; Pred. No. 48; 0; Mismatches 1; Indels 0;
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/mol_type="mRNA"
/cultivar="TA496"
1. .473
/organism="Medicago truncatula"
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                                       'mol_type="mRNA"
'db_xref="taxon:3880"
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/clone="cLEC71G2"
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                                                                                clone="NF092E03IR
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Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library.
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(Efranch-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, P.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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148 c 165 g 187 t 2 others
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01894, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                Score 22.4; DB 12; Length 597; Pred. No. 51; 0; Mismatches 1; Indels 0;
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
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us-10-082-772-4.rst

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A genomic sample sequence of the entomopathogenic bacterium bytcorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                       South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Exa: (44) 1225 826779
Email: bestfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG00827, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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158 c 169 g 200 t 2 others
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/organism="Photorhabdus luminescens"
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                                                                                                               Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
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Biochemistry
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Pred. No. 55;
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Rfc00827 Photorhabdus luminescens
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/strain="W14"
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/clone="PLG01106"
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Department of Biology and Bioche
University of Bath
South Building, Bath BA2 7AY, UI
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Class: shotgun.
Location/Qualifiers
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95.8%;
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ifrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 82679
Email: bssrfc@bath.ac.uk
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                                                                                                                                                                                                          Sacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Enterobacteriaceae, Photorhabdus.
                 AQ990809
Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01638, genomic survey
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Rfc01106 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
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/clone="PLG01638"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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    712
/organism="Photorhabdus luminescens"

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1 (bases 1 to 712)
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/strain="W14"
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Class: shotgun,
Location/Qualifiers
                                                                                                                                                                   Photorhabdus luminescens
Photorhabdus luminescens
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AQ990809.1 GI:9649403
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 395)
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Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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llarity 91.7%; Pred. No. 1.2e+02;
Conservative 0; Mismatches 2;
                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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                                                                         DВ
                                                                       Score 22.4; DE
Pred. No. 55;
0; Mismatches
            204 t
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/clone="PLG02205"
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                                                                                                                                                    1 CAACTTAGTATCAAAAAGCTGAAC 24
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                מ
            174
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Photorhabdus luminescens
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                                                                       93.3%;
              U
                                                                                                            23; Conservative
            163
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Best Local Similarity
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            223 a
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                                                                    Query Match
Best Local S:
Matches 23
                                                                                                                                                                                                                                                  RESULT 12
AQ991303
LOCUS
DEFINITION
          BASE COUNT
ORIGIN
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AQ989566
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KEYWORDS
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firench-Constant, R.H., Materfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
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/dev_stage="primary phase variant"
/dov_lone_lib="Photorhabdus luminescens strain W14 M13
library.
/note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
                                                                                                                                                                                                    /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
|ibrary"
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                                                                                                    'organism="Photorhabdus luminescens"
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Department of Balology and Blochemistry
University of Bath
South Building, Bath BA2 7AY, UK
T=1: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                     Score 22.4; DB
Pred. No. 55;
0; Mismatches
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                                                                                                                         mol_type="genomic DNA'
strain="W14"
                                                                                                                                                              db_xref="taxon:29488"
clone="PLG00827"
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                    Seg primer: M13 Forward
Class: shotgun.
Location/Qualifiers
1. .764
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Class: shotgun.
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95.8%;
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Acids Res.
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Acids Res.
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Best Local S.
Matches 23
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LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 AQ990470

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ORGANISM

REFERENCE AUTHORS MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

BASE COUNT ORIGIN

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source

FEATURES

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

MEDLINE PUBMED

JOURNAL

TITLE

DEFINITION

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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
146 c 161 g 179 t 2 others
                                                                                            Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Famil: bestreabsth.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence 203386331.
203386331.
10919786
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Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Photorhabdus luminescens genomic clone PLG01698, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:29488"
/clone="PLG01701"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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                     Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .672
/organism="Photorhabdus luminescens"
/mol type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%; Score 20.8; DB 28;
91.7%; Pred. No. 2.5e+02;
live 0; Mismatches 2;
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae, Photorhabdus.
1 (bases 1 to 753)
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Class: shotgun.
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Seq primer: M13 Forward
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AQ990861.1 GI:9649455
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Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library"
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KEYWORDS
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AQ990861
LOCUS
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                                                                                                                                                                                                                                                                     (bases 1 to 751)

(Efrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. Banomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, P.R.
A genomic sample sequence of the encomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
                                                                                                                                                           Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Rfc00126 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00126, genomic survey
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Rfc01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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89.2%; Score 21.4; DB 28; Length 751;
Best Local Similarity 91.7%; Pred. No. 1.46+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0;
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
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South Building, Bath
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Photorhabdus
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clone="PLG00126"
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Class: shotgun.
Location/Qualifiers
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Photorhabdus luminescens
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RESULT 14 AQ990864 LOCUS DEFINITION

BASE COUNT

ORIGIN

FEATURES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

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Gaps

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GSS 14-AUG-2000

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us-10-082-772-4.rst
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Class: shotgun.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Lorans="Photorhabdus luminescens"

Mol_type="genomic DNA"

Ado_reage="primary phase variant"

Ado_reage="primary phase variant"

Alone="Genomic DNA from strain W14 M13

Library"

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

Anote="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was size selected (1-2 kb) and then cloned into M14 was
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Search completed: December 3, 2003, 14:49:19 Job time : 1076.23 secs

Appl Appl Appl Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence

Sequence

Sequence

Sequence

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Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

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Sequence 18, Application US/08021667A

Patent No. 5434049

GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.4; DB 1; Length 201; Pred. No. 0.28; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: DC.
COMPUTER: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC.
COUNTRY: USA
ZATE: DC.
COMPUTER: DC.
COMPUTER: PREADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PATENTIN BATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 1993024
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: TELEVOMORISE: 202,178
REGISTRATION NUMBER: 20,178
REGISTRATION NUMBER: 520,178
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEXX: 202-828-0380
               US-09-312-283C-203
US-08-486-013-69
US-08-342-268-69
US-09-307-386-69
US-09-307-386-69
US-09-308-090-1
US-09-380-090A-1
US-09-068-101-10
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US-09-233-493-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%;
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                   Query Match
Best Local Similarity
Matches 23; Conserv
                   US-08-021-667A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-021-667A-18
22666666666666444444
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                                                                                                                      3, 2003, 12:13:45; Search time 28.562 Seconds (without alignments) 370.884 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, All
Sequence 43, 7
Sequence 42, 7
Sequence 7, All
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Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgm2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
           version 5.1.6 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-021-667A-18

US-08-410-544-18

US-08-556-978B-78

US-09-296-280-43

US-09-296-280-43

US-09-296-280-43

US-09-296-280-43

US-09-685-15-17

US-09-685-15-17

US-09-296-280-15

US-09-296-280-15

US-09-296-280-15

US-09-296-280-15

US-09-296-280-15

US-09-296-280-15

US-09-296-280-15

US-09-296-280-17

US-09-296-280-11

US-09-296-280-39

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US-09-296-280-39

US-09-296-280-39

US-09-296-280-39

US-09-296-280-39

US-09-296-280-39

US-09-296-280-30

US-09-296-280-30

US-09-296-280-30

US-09-108-30-30
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   569978 segs, 220691566 residues
                                                                                                                                                                                                                                       1 gttcagctttttgatactaagttg 24
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
             GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
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Match Length DB
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24
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Maximum DB
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Gaps

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STREET: Suite 180
CITY: Arlington
STATE: VA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
US-08-728-785A-18
                                                                                                                                                                                                                                                                               22209
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                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kambara, Hideki
NENTION: POLYNUCLEOTIDE CAPTURING TIP AND
VENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
VENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 0.28;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
FILING DATE:
CLASSIFICATION 1435
PRICA APPLICATION NUMBER: 08/021,667
PILING DATE: 24-FEB-1993
ATTONREY/AGBRT INPORMEX: 08/021,667
PILING DATE: 24-FEB-1993
ATTONREY/AGBRT INPORMEX: 08/021,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Antonelli, Terry, Stout & Kraus STREET: Suite 600, 1919 Pensylvania Ave., NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520.31930X00
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US-08-728-785A-18
'S Gquee 18, Application US/08728785A
'Patent No. 5817506
                                                                                                                                                                                                                                                                Sequence 18, Application US/08410544
Patent No. 5607646
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMULICATION NUMBER: 20,178
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520,3
TELEPHONE: 202-828-0380
TELEX: 248545
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear NOLECULE TYPE: DNA (genomic) NUMBER: 10,100 NUMBER: 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%;
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Okano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: DC
                                                                                                                                                                                                                        US-08-410-544-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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DB 1; Length 201;
E: Antonelli, Terry, Stout & Kraus
Suite 1800, 1300 No. 5817506th Seventeenth St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILING DATE: U-OCT-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,544
FILING DATE: 1-MAR-1995
PRIOR APPLICATION NUMBER: 08/21,667
FILING DATE: 21-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terry David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELERCOMMUNICATION INFORMATION:
TELERCAX: 703-312-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FAHNEGTOCK, STEPHEN F.

TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STRET: 107) MARKET STREET
CITY: MILMINTON
STATE: DELAMARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WOND FOR WINDOWS 95
CURRENT APPLICATION DATA: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 GTTCAGCTTTTTTATACTAAGTTG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELAWARE
                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KESULT.
US-08-556-978B-78/c
; Sequence 78, Application US/08556978B
: Patent No. 6268169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTTCAGCTTTTTGATACTAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.3%;
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.8
Matches 23; Conservative
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nucleic acid
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FARENL NO. 22.7/00/8.

APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Tarple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: NOWHER: US/09/296,280
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1998-04-22
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER PILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                   Length 7652;
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                                        Query Match
93.3%; Score 22.4; DB 1;
Best Local Similarity 95.8%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21.2;
Pred. No. 0.8
                                                                                                                                                                                            6071 Girchichirirahachadrig 6094
                                                                                                                                                 TTGATACTAAGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITCAGCTITITGATACTAAGTIG 24
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                                                                                                                                                                                                                                                                    RESULT 6
US-09-256-280-43
Sequence 43, Application US/09296280
Patent No. 6277608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09296280
Patent No. 6277608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Unknown
US-07-590-988A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-296-280-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-296-280-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.3%; Score 22.4; DB 3; Length 4909; Best Local Similarity 95.8%; Pred. No. 0.32; Matches 23; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800%b storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/07590988A
Parent No. 5227288
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Sequencing Vector with
TITLE OF INVENTION: Reversible Insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Other nucleic acid, DESCRIPTION: synthetic recombinant plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2378 Gircagcriririraracraagrig 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629691682
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SUFTWARE: Microsoft Word 4.0
UNDERNIT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,988A
FILING DATE: 19901001
                                                                                                                                                                                            CR-9389-A
       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,60(
FILING DATE: JUNE 15, 1933
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles and Brady
STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
                                                                                                                                                                                                                                                       TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 4909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-556-978B-78
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WISCONSIN
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: MADISON STATE: WISCONSI COUNTRY: U.S.A.
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US-09-655-728-7
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FEATURE:
7 OTHER INFORMATION: Description of Unknown Organism: recombination US-09-296-280-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08894511
Fatent No. 6143530
GENERAL INFORMATION:
APPLICANT: SCHERMAN, Daniel
APPLICANT: SCHERMAN, Daniel
APPLICANT: SCHERMAN, Baatrice
APPLICANT: WILS, Pierre
APPLICANT: W
                                                                                                                                                                                                    85.0%; Score 20.4; DB 3; Length 25; Larity 75.0%; Pred. No. 1.9; Conservative 5; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/02117
FILING DATE: 23-FEB-1995
PRIOR APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
TELEPHONE: (610) 454-3816
TELEPHONE: (610) 454-3808
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENOTH: 21 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonuclectide"
                                                                                                                                                                                                                                                                                                                                                                   1 GTTCAGCTTTTTGATACTAAGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTYTTRACWAASTKG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCITITIGATACIAAGIIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
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                                                                                                                             WILS, Pierre
DARGUET, Anne-Marie
DARGUET, Anne-Marie
TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
USE THEREOF IN GENE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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US-09-233-493-15
US-09-233-493-15

Sequence 15, Application US/09233493

Patent No. 6143557

GENERAL INFORMATION:

APPLICANT: Harsch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                               CUCNAIRS: USA,
CUCNAIRS: USA,
CUCNAIRS: LODA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/655,728
FILING DATE: 05-Sep-2000
CLASSIFICATION OTAA:
APPLICATION NUMBER: 08/894,511
FILING DATE: CURNOWN>
APPLICATION NUMBER: WF.96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: SAVITEXY ESQ:, MARTIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION AF4-3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Pred. No. 5.
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Sequence 7, Application US/09655728
Patent No. 6492164
GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
SCHERMAN, Daniel
CAMERON, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCTTTTTATACTAAGTTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.2
Matches 20; Conservative
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FILING DATE: herewith
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TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-233-492-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-233-492-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-1934
COMPUTER: READBAILE FORM:
MEDIUM TYPE: Flopsy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/005,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                    SEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
: 1100 New York Ave., N. W. Suite 600
Washington
                                                                                                                                                                                                               CONTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493

FLING DATE: 20-JAN-1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002

FLING DATE: 07-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1996

CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1996

CLASSIFICATION:
CLASSIFI
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80.0%; Score 19.2; DE
Best Local Similarity 87.5%; Pred. No. 6.5;
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTTCAGCTTTTTGATACTAGGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Grrcagcriririrgracaaagrig 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-005-476-15; Sequence 15, Application US/09005476; Patent No. 6111861; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-15
                                                                                                                                                                                                   USA
                                                                                                                                                          STATE: DO
                                                                                 STREET:
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Filture Date: necessarian

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Filture Date: 00/453,002

FILIRO DATE: 00/478/196

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FILIRO DATE: 00/478/196

FILIRO DATE: 00/478/196

FILTURE DATE: 00/47/196

FILTER DATE: 00/47/196

FILTURE DAT
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APPLICANT: Life Technologies, Inc.
APPLICANT: B17 Growemort Circle
APPLICANT: Wile States of America
APPLICANT: B17 Growemort Circle
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE
STRPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 19.2; DB 4; Length 25; 87.5%; Pred. No. 6.5;
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ZIP: 20005-3934

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OOMPATING SYSTEM: PC-DOS/NS-DOS
OOFFWATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A

TITING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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                                                                                                                                                                                                                 PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRILING DATE:
PILLING DATE:
PILLING DATE:
PRICEPHONE:
TELEPHONE:
TELEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GITCAGCTITITGAIACTAAGTIG 24
                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-371-2600
TELEPRAX: 202-371-2540
INFORMATION FOR SEQ ID NO. 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.08;
                                                         12-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 25 base pairs
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STRANDEDNESS: both
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT PRING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER PILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
                                                         Gaps
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Sequence 15. Application US/09498074
Fatent No. 6534264
Fatent Hartley, James L.
FAPLICANT: Branch, Michael A.
FITLE OF INVENTION: Recombinational Cloning Using Engineered
FITLE OF INVENTION: Recombination Sites
FATES OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
FATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: recombination // OTHER INFORMATION: products
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80.0%; Score 19.2; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 6.5;
Matches 21; Conservative 0; Mismatches 3; Indels
                                                  3; Indels
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
87.5%; Prec. ....
                                                                                                                       1 GITCAGCTITITGATACTAAGTIG 24
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Patent No. 6277608
                                                  Conservative
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          Best Local Similarity
Matches 21; Conserv
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                      US-09-296-280-15
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LENGTH: 25
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ö 0; Gaps 3; Indels Best Local Similarity 87.5%; Pred. No. 6.5; Matches 21; Conservative 0; Mismatches

1 GTTCAGCTTTTTGATACTAAGTTG 24

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Search completed: December 3, 2003, 14:51:46 Job time: 29.562 secs

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Expression vector
Expression vector
Expression vector
E. coli attp* DNA
Phage-lambda recom
Attp DNA fragment.
Att site nucleotic
Detection probe 11
                                                                                                                                                                                            December 3, 2003, 12:13:41; Search time 114.843 Seconds (without alignments) 564.131 Million cell updates/sec
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5: SIDSI/gogdata/geneseqn-embl/NA1981.DAT:
6: SIDSI/gogdata/geneseqn-embl/NA1981.DAT:
7: SIDSI/gogdata/geneseqn-embl/NA1981.DAT:
8: SIDSI/gogdata/geneseqn-embl/NA1981.DAT:
9: SIDSI/gogdata/geneseqn-embl/NA1991.DAT:
9: SIDSI/gogdata/geneseqn-embl/NA1992.DAT:
9: SIDSI/gogdata/geneseqn-embl/NA1992.DAT:
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9: SIDSI/gogdata/geneseq/geneseqn-embl/NA2000.DAT:
9: SIDSI/gogdata/geneseq/geneseqn-embl/NA2001B.DAT:
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9: SIDSI/gogdata/geneseq/geneseqn-embl/NA2001B.DAT:
9: SIDSI/go
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sescription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_19Jun03:*
. /SIDSI/gogdata/geneseq/geneseqn-embl/NA1980.DAT:*
: /SIDSI/gogdata/geneseq/geneseqn-embl/NA1981.DAT:*
: /SIDSI/gogdata/geneseq/geneseqn-embl/NA1982.DAT:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2552756 segs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          1 gttcagctttttgatactaagttg 24
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Maximum Match 100%
Listing first 45 summaries
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AAF61421
AAF61421
AAS06175
AAF61424
ABZ58728
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                            US-10-082-772-3
                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                           Run on:
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Bacteriophage lamb Murine rDNA PCR pr Artificial plant c Bacteriophage lamb Rat neuronal immed Plasmid pSY40193at Artificial plant c	772222	tt site mucleot coli attR DNA ligomucleotide acteriophage la ucleotide core utational attL OR primer attLT ELPI core regio	cleotid cleotid mation ration chia co quence nation	Att mite molectid Attificial plant c Phage-lambda recom Phage-lambda recom Phage-lambda recom
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220522	9 2 2 2 2 4 5 2	12222	000000000000000000000000000000000000000	5555 5555 5555
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## ALIGNMENTS

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Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect
                                                                                              Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; attP*; PCR primer; ss.
                                                                       Expression vector pXEX-2-XR attP and attP* PCR primer 03
          AAF61394 standard; DNA; 24 BP
                                                                                                                                                                                                99DE-1041186
                                                                                                                                                                                                                     30-AUG-1999; 99DE-1041186
                                                   05-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                    WPI; 2001-246016/26.
                                                                                                                                                                                                                                         (DROE/) DROEGE P.
                                                                                                                                                    DE19941186-A1.
                                                                                                                                                                                                30-AUG-1999;
                                                                                                                                                                          01-MAR-2001.
                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                Droege P;
                                AAF61394;
AAF61394
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This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 5 A; 3 C; 5 G; 11 T; 0 other;
recombination between att sites
                                                      Example 1; Page 8; 24pp; German.
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Gaps ö DB 22; Length 24; Indels . 0.28; 100.0%; Score 24; DB 100.0%; Pred. No. 0.2 ive 0, Mismatches 1 GITCAGCTITITGATACTAAGTIG 24 24 Gircagciriridaraciaagirg 24; Conservative Query Match Best Local Similarity Matches 24; Conserv à 원

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AAF61395 standard; DNA; 24 RESULT 2 AAF61395/c 

AAF61395;

Expression vector pKEX-2-XR attP and attP\* PCR primer 04.

(first entry)

05-JUN-2001

Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP\*; PCR primer; ss.

Synthetic.

DE19941186-A1

01-MAR-2001

99DE-1041186 30-AUG-1999;

99DE-1041186, 30-AUG-1999;

(DROE/) DROEGE

Droege P;

WPI; 2001-246016/26

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -

Example 1; Page 8; 24pp; German.

This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (int) to effect SSR. The invention also describes (I) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy it derivatives. The method is applied more generally for gene theraper to animals or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.

1 GITCAGCITITIGATACTAAGTIG 24

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AAF61421 standard; DNA; 243

RESULT 4

AAF61421

AAF61421 ID AAF XX AC AAF XX

Sequence 24 BP; 11 A; 5 C; 3 G; 5 T; 0 other

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                                                                                                                                                                                                                                                                Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP*; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel sequence-specific recombination (SSR)
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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      Length 24;
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0
    DB 22;
0.28;
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100.0%; Pred. No. 0.28;
ive 0; Mismatches 0;
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                                 0; Mismatches
    100.0%; Score 24;
                                                            1 GITCAGCITITIGATACTAAGTIG 24
                                                                                  GTTCAGCTTTTTGATACTAAGTTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 6B; 24pp; German.
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                                                                                                                                                               AAF61425 standard; DNA; 27
Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                  AttP* DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DROE/) DROEGE
                                                                                                                                                                                                                                                                                                                                                     DE19941186-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1999;
                                                                                                                                                                                                                                                                                                                          Unidentified
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09-MAR-2000; 2000US-0188020.
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                         CHEO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                                                                                                          This invention describes a novel sequence-specific recombination (SSR) of
                                                                                                                                                                                                                                                                                                 DNA in a enkaryotic cell, conversing introducing two DNA sequences (1, 11) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                              Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                         Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attp*; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
lambda integrase; therapeutic; ss.
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Pred. No. 0.33;
; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 243 BP; 74 A; 34 C; 34 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIICAGCIIIIIGAIACIAAGIIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phage-lambda recombination site atP01
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTTTGATACTAAGTTG 24
                                                                                                                                                                                                                                                                      Claim 19; Page 14; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
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nes 24; Conservative (
                                                                                                                                99DE-1041186
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                     E. coli attP* DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS06175 standard; DNA; 27
05-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sacteriophage lambda;
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                                                                     Escherichia coli.
                                                                                                                                                                     (DROE/) DROEGE
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                                                                                       DE19941186-A1
                                                                                                                               30-AUG-1999;
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                                                                                                          01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-2001
                                                                                                                                                                                         Droege P;
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                                                                                                                                                                                                                                                                                              Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-specific recombination; SSR; integrase; gene therapy; somatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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                                                                                                                                                                                Byrd DRN;
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Pred. No. 1.4;
0; Mismatches 1;
                                                                                                                                                                             Temple GF, Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 6 A; 4 C; 5 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTTCAGCTTTTTGATACTAAGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gricagciririrahactaagirg 24
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 24A; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :wo or more different nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       targeted integration; attP; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF61424 standard; DNA; 27 BP
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nes 23; Conservative
CHEO D.
BRASCH M A.
TEMPLE G F.
HARTLEY J L.
                                                                                                                                                                             Brasch MA,
                                                                                                                                                                                                                                       WPI; 2001-356174/37.
                                                                                                                   BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AttP DNA fragment
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                                                      (TEMP/)
(HART/)
(BYRD/)
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form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. Sequences ABZ58727-762 represent att recombination site sequences used in the method of the

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Gaps

.. 0

Length 27; Indels

25; 1;

Score 22.4; DB Pred. No. 1.4; 0; Mismatches

ch 93.3%; 1 Similarity 95.8%; 23; Conservative (

Best Local Similarity Matches 23; Conserv

Query Match

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1 GITCAGCTTTTGATACTAAGTTG 24

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Sequence 27 BP; 6 A; 4 C; 5 G; 12 T; 0 other;

invention

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This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sommatic gene therapy its derivatives. The method is applied more generally for gene transfer to animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
               DNA in eukaryotes, useful
therapy, uses an integrase to effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                      93.3%; Score 22.4; DB 22; Length 27; 95.8%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                       Sequence 27 BP; 6 A; 4 C; 5 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                1 GITCAGCTITITGATACTAGTIG 24
                                                                                                                                                                                                                                                                                                                                                                                    GITCAGCITITITATACTAAGTIG 24
              Sequence-specific recombination of particularly for somatic cell gene recombination between att sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Att site nucleotide sequence attPO.
                                                                       Disclosure; Fig 6B; 24pp; German
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                                                                                                                                                                                                                                                                                                                   Local Similarity 95.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-129436/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                     Query Match
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AB258728
ID AB25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAO50309-26 are probes which were used on a chip for capturing a number of target polynuclectides. A group of these probes may be attached on cells which form part of a single chip. The oligonuclectides to be detected are labelled and are complementary to the set of capture probes used. The detection ch may be used to detect a number of different polynuclectides
                                                                                                                                                                                                                                                                                                                                                                                Chip for capturing polynucleotide - has several different complementary probes fixed on cells at different sites on single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22.4; DB 14; Length 201; Pred. No. 1.6; 0; Mismatches 1; Indels 0
                                                                                                                                                                      Probe; chip; cell; detection; label; capture probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 other;
GricaGcriririanachagirg 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GITCAGCTITITGATACTAAGTIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GIICAGCITITITATACTAAGITG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 10pp; Japanese.
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Best Local Similarity 95.8%;
Matches 23; Conservative
                                                                AAQ50319 standard; DNA; 201
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                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                             (HITA ) HITACHI LTD.
                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-330600/42.
                                                                                                                                             Detection probe 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concurrently.
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                                                                                                                                                                                               Synthetic.
                                                                                          AAQ50319;
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                                     KESULT 8
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AAF61418
ID AAF6
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AC AAF6
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid of nucleic acid with a second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to

Disclosure; Fig 13A; 273pp; English.

05-JUN-2001 (first entry)

99DE-1041186

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DNA in a eukaryotic cell, comprising introducing two DNA sequences (1, 11) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a novel sequence-specific recombination (SSR) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
                                                         Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                                                                                                                                                                                                                                                                       Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 other;
                           Bacteriophage lambda attP DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 13; 24pp; German.
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                                                                                                    Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                             WPI; 2001-246016/26.
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                                                                                                                                                                                                                                                  (DROE/) DROEGE
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                                                                                                                                                           01-MAR-2001
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                                                                                                                                                                                                                                                                                Droege P;
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Matches
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits sites, where an att site is heterologous to the chromosome ambod-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a ransgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid mediated transfection, marcopojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                 Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                               Fleming E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 22.4; DB 25; Length 282; 95.8%; Pred. No. 1.7; 1; Indels 0
                                                                                                                 Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other;
                                                                                                               Greene A,
                                                                       (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 GTTCAGCTTTTTTATACTAAGTTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GITCAGCTTTTTGATACTAGTTG 24
                                                                                                             Lindenbaum M,
                                                                                                                                                                                                                                                                                             Example 2; Page 207; 272pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT16636 standard; DNA; 282 BP
                 30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2002; 2002WO-US17451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2001; 2001US-294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 95.8<sup>3</sup>
Matches 23; Conservative
                                                                                                         Perez C, Li
Shellard J;
                                                                                                                                                               WPI; 2003-140461/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200296923-A1
                                                                                                         Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35-DEC-2002
                                                                                                                                                                                                                                                             interest
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ABT16636
à
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Gaps ; 0

Score 22.4; DB 22; Length 243; Pred. No. 1.7; 0; Mismatches 1; Indels 0;

93.3%;

23; Conservative

dricadciririrataciaagirg 162

30-MAY-2002; 2002WO-US17452;

24

1 GITCAGCITITIGATACTAAGIIG

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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ENRA, rDNA, structural proteins, marker proteins, isgands, receptors, ribozymes, therapeutic proteins, and product proteins, lagands, receptors, ribozymes, blood factors, antigens, hormones, ovtokines, growth factors, antigeds, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid alterial acid acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This producing plant artificial chromosomes of the invention.
                                                                                                                                                                                                                                       Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 263-264; 269pp; English.
                                                      CHROMOS MOLECULAR SYSTEMS INC
                                                                                                                                     Perkins E;
  04-JUN-2001; 2001US-296329P
                                                                                                                                Perez C, Fabijanski SF,
                                                                                 AGRISOMA INC
                                                                                                                                                                                      WPI; 2003-140436/13
                                                      CHRO-)
                                                                                 (AGRI-)
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Score 22.4; DB 25; Length 282; Pred. No. 1.7; 1; Indels 0; Mismatches 24 1 GTTCAGCTTTTTGATACTAAGTTG 93.3%; 95.8%; 23; Conservative Similarity Query Match Best Local S ठे

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Gaps

; 0

Gricagciririrahactaagrig 176 153 a

AAF79770 standard; DNA; 610

ВБ. (first entry) 29-MAY-2001 AAF79770; 

Bacteriophage lambda attachment F region.

Attachment P region; attP; recombination; marker gene removal; ds.

Bacteriophage lambda.

WO200121780-A2

29-MAR-2001.

15-SEP-2000; 2000WO-GB03543

99GB-0021937 17-SEP-1999;

(UYLE-) UNIV LEEDS.

Meyer P,

WPI; 2001-266072/27

Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene

8; Fig 3D; 25pp; English. Claim

The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attp) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antiblotic resistance. The present sequence is the attP coding region.

Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 other;

Gaps ; 0 Score 22.4; DB 22; Length Pred. No. 1.8; 1; Indels 0; Mismatches ch 93.3%; 1 Similarity 95.8%; 23; Conservative C Best Local Similarity Query Match Matches

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AAZ30709 standard; cDNA; 1763

05-JAN-2000 AAZ30709;

(first entry)

Rat neuronal immediate early gene cDNA clone R280.

Immediate early gene, IEG; neuron; brain; function; growth factor; transcription factor; signal transduction; cytoskeletal protein; metabolic enzyme; learning; memory; synaptic transmission; tolerance; neuronal plasticity, ds.

Rattus sp.

WO9940225-A1

12-AUG-1999

99WO-US02462. 05-FEB-1999;

98US-0074135. 09-FEB-1998; 12-FEB-1998;

(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE. (BADI ) BASF-LYNX BIOSCIENCE AG.

Kuner R, Hiemisch H, Goetz B, Lanahan A, Go Zhukovski E; Worley PF, Nikolich K,

WPI; 1999~590697/50

Novel genes and polypeptides, useful for treating conditions related to a deficiency in nIEG responsiveness to a stimulus

Claim 1; Page 114-115; 134pp; English.

This sequence represents rat neuronal immediate early gene (IEG) cDNA clone R280. An IEG is a gene whose expression is rapidly increased immediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode a variety of proteins, including transcription factors, cycoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal RESULT 13
AAZ30709/c
ID AAZ30709/c
XX AAZ30
DT 05-JA
DX Rat n
XX Immed
KW Immed
KW Metab
KW Metab
KW Metab
KW MO994
XX RATTU
XX RO99-FE
XX O9-FE
XX (UYJC
PR 05-FE
XX (UYJC
PR 05-FE
XX (UYJC
PR 12-FU
XX (UYJC
PR 13-FU
XX (UYJC
PR

transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in for scample. Learning, memory, synaptic transmission, colerance and neuronal plasticity. Neuronal IEGs, neuronal IEG protein products, cells expressing neuronal IEGs and antibodies against neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG minimised. The deficiency way be a reduced or elevated level of expression of an IEG. The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IESs and protein products are useful in identifying compounds that modulate the expression or activity of IEG nucleic acids or proteins, respectively. \$

Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 7 other;

Gaps . 0 Score 22.4; DB 20; Length 1763; Pred. No. 1.9; 0; Mismatches 1; Indels 0; Indels ; 1 93.3%; Query Match
Best Local Similarity 95.00.

293 Gircagciririraraciaagirg 270 GITCAGCITITIGATACTAAGITG 24

ò 셤 RESULT 14

ACC44716

ACC44716 standard; DNA; 4346 BP.

ACC44716;

(first entry) 29-MAY-2003

Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.

Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.

Bacteriophage lambda

Synthetic

WO200297059-A2

05-DEC-2002

30-MAY-2002; 2002WO-US17452

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

Greene A, Leung J, Fleming Lindenbaum M, Perez C, Li Shellard J; Perkins E, Stewart S,

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WPI; 2003-140461/13.

permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of eukaryotic chromosome comprising one or many att sites which interest Novel

Example 3; Page 244-245; 272pp; English.

The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is hererologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for 

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introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinfoction, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of Aces comprising random portions of a genome. ACC44612 to ACC446122 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
   886666666666888
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Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other;

Gaps ·; Length 4346; 1; Indels ch 93.3%; Score 22.4; DB 25; Similarity 95.8%; Pred. No. 2; 23; Conservative 0; Mismatches 1; Query Match Local Matches

0

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RESULT 15 ABT16615

ABT16615 standard; DNA; 4346 BP.

ABT16615;

03-APR-2003 (first entry)

Artificial plant chromosome related plasmid DNA SEQ ID No 26.

Plant artificial chromosome, PAC; transgenic plant; vaccine, blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;

Unidentified.

WO200296923-A1.

05-DEC-2002.

30-MAY-2002; 2002WO-US17451

30-MAY-2001; 2001US-294687P.

CHRO-) CHROMOS MOLECULAR SYSTEMS INC. AGRI-) AGRISOMA INC.

Perkins Perez C, Fabijanski SF,

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WPI; 2003-140436/13.

Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids

Example 19; Page 255-256; 269pp; English.

The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, back, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and blopharmaceutical proteins, vaccines, blood factors, antigens, hormones, 

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cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nuclaic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents the DNA of a plasmid used in the method of the invention.
      88888888888
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Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other;

Gaps 0; Query Match
Best Local Similarity 95.8%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 1; Indels 0;

g 8

Search completed: December 3, 2003, 12:23:35 Job time : 114.843 secs

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Sequence 3, Appli
Sequence 4, Appli
Sequence 26, Appli
Sequence 72, Appli
Sequence 77, Appl
Sequence 57, Appl
Sequence 13, Appl
Sequence 43, Appl
Sequence 44, Appli
Sequence 28, Appl
Sequence 28, Appli
                                                                                           December 3, 2003, 13:18:51; Search time 107.107 Seconds (without alignments) 744.732 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 US-10-151-690-26

2 US-09-248-05-57

2 US-09-248-05-57

3 US-10-161-403-113

3 US-09-855-7978-43

3 US-09-985-448-43

4 US-10-151-690-28

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4 US-09-855-7978-42
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US-10-082-772-4
US-09-732-914-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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24
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Perfect score:
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Maximum DB
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                                                                                              Run on:
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US-09-907-900-42 US-09-908-48-48-42 US-10-300-892-42 US-10-20-384-7 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	3-10-151-690 3-10-151-690 3-10-151-690 3-10-151-690
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22 22 22 22 22 22 22 22 22 22 22 22 22	27 27 27 44 70
4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 4 4 4 4

## ALIGNMENTS

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US-10-082-772-3/C

US-10-082-772-3/C

US-10-082-772-3/C

PUBLICARTED NO. US20030027337A1

GENERAL INFORMATION:

APPLICANT: CHRIST, NICOLE

APPLICANT: CHRIST, NICOLE

APPLICANT: CRORAGE, BETER

TITLE OF INVANITON: SEQUENCE-SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS

FILE REPRENEUR: DESE: 000-00-29

PRIOR FILING DATE: 2002-65-21

PRIOR FILING DATE: 1999-08-30

MUMBER OF SEQ ID NOS: 20

SOTTWARE: Patentin Ver. 2.1

SEQ ID NO 3

SOTTWARE: Patentin Ver. 2.1

SEG ID NO 3

SOTTWARE: Patentin Ver. 3

SEG ID NO 3

SOTTWARE: Patentin Ver. 3

SEG ID NO 3

SOTTWARE: Patentin Ver. 3

SOTTWA
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APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: DOMINIC
APPLICATION NUMBER: US.10/1151,690
CURRENT PILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 26
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22.4; DB 14; Length 27; Pred. No. 1.6; 0; Mismatches 1; Indels C
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APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Fleming Elena
APPLICANT: Fleming Elena
APPLICANT: Shewart, Sandra
APPLICANT: Shewart, Joan
ITILE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: 60/294,758
FRICH APPLICATION NUMBER: 60/294,758
FRICH APPLICATION NUMBER: 60/294,758
FRICH FILING DATE: 2001-05-30
FRICH APPLICATION NUMBER: 60/366,891
FRICH FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 72, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.3%;
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                                                  APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.00
The 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.8
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: attp
US-10-161-403-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: attP0
US-10-151-690-26
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US-09-244-805-57
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Sequence 2, Application US/09732914

Sequence 2, Application US/09732914

Sequence 2, Application US/090007051A1

GENERAL INFORMATION:

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Byrd, Devon R.N.

TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Use combinational Cloning

FILE REFERENCE: 0942.501002

CURRENT PELLORY NUMBER: US/09/732,914

PRIOR PPLICATION NUMBER: US 60/169,983

PRIOR FILING DATE: 2000-12-10

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SOFTWARE: PatentIn version 3.0

LEATH: 27

LEATH: 27

LEATH: 27
                                                     APPLICANT: DROGE, PETER
APPLICANT: DROGE, PETER
APPLICANT: CHRIST, NICOLE
APPLICANT: CHRIST, NICOLE
APPLICANT: CHRIST, NICOLE
APPLICANT: LORDANCH, EMBACH, EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-10-082-772-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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95.8%; Pred. No. 1.6;
tive 0; Mismatches 1;
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US-10-151-690-26/c
; Sequence 26, Application US/10151690
; Publication No. US20030124555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
Publication No. US20030027337A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
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Best Local Similarity
Matches 23; Conserv
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ORGANISM: attP0
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Greene, Amy
APPLICANT: Fleung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REPERRNCE: 24601-450
CURRENT APPLICATION NUMBER: US/10/161,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: pSV40-193AttpsenseFur Plasmid
US-10-161-403-113
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                      270 caactingininaaaaaadcicaac 293
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                                                 1 CAACTTAGTATCAAAAAGCTGAAC 24
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                                                                                                                                                                                                                                     Sequence 113, Application US/10161403
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                                                                                                                                                                                                                                                           Publication No. US20030119104A1
GENERAL INFORMATION:
  23; Conservative
                                                                                                                                                                                                                                                                                                                APPLICANT: Perkins, Edward
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                                                                                                                                                                                                               -403-113/c
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  Matches
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Publication No. US20030211984A1
GENERAL INFORMATION.
APPLICANT: Worley, Paul F.
APPLICANT: Unablan, Anthony
TITLE OF INVENTION: INMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: INMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: INMEDIA: US/09/245,277
CURRENT APPLICATION NUMBER: 06/074,518
PRIOR PILICATION NUMBER: 60/074,518
PRIOR PILICATION NUMBER: 60/074,135
PRIOR PILICATION NUMBER: 60/074,135
NUMBER OF SEQ ID NOS: 63
SOFTWARR: FASTERED for Windows Version 4.0
                                                            GRENEAL INFORMATION:

APPLICANT: Worley, Paul F.

APPLICANT: Lanahan, Anthony,

APPLICANT: Lanahan, Anthony,

APPLICANT: Gener, Bernard

APPLICANT: Runer, Rohini,

APPLICANT: Kuner, Rohini,

APPLICANT: Kuner, Rohini,

APPLICANT: Scheek, Sigrid

APPLICANT: Chukovski, Eugene

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: IMMESER: 06/04001

CURRENT FALING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/074,518

EARLIER PILING DATE: 1999-02-06

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.3%; Score 22.4; DB 12; Length 1763; Best Local Similarity 95.8%; Pred. No. 3.7; Matches 23; Conservative 0; Mismatches 1; Indels 0;
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CTHER INFORMATION: y = C or T

OTHER INFORMATION: n = A,T,C or G
Sequence 57, Application US/09244805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(1763); OTHER INFORMATION: y = C or T ; OTHER INFORMATION: n = A,T,C or G US-09-244-805-57
                        Publication No. US20030203840A1
GENERAL INFORMATION:
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ORGANISM: Eukaryote
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US-09-245-277-57
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APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285008
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 2001-05-16
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 25
                                                    Gaps
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Length 4346;
                                                    Indels
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us-10-082-772-4.rnpb

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APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Mucleic Acids Having TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TILE OF INVENTION WINBER: US/09/985,448
CURRENT FILING DATE: 1990-11-02
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR APPLICATION NUMBER: US 60/065,930
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 43
LENGTH: 25
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APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION NUMBER: US/10/300,892
CURRENT FILING DATE: 2001-02-11-21
PRIOR PILING DATE: 2001-07-19
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
                                                                                                                           Gaps
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OTHER INFORMATION: Description of Unknown Organism: recombination
US-09-985-448-43
                                                                88.3%; Score 21.2; DB 10; Length 25; 83.3%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.3%; Score 21.2; DB 12; Length 25; 83.3%; Pred. No. 5.6;
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                                                                                                                   3; Mismatches
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Publication No. US20030157716A1
GENERAL INFORMATION:
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Publication No. US20030175970A1
GENERAL INFORMATION:
                                                                                      Best Local Similarity 83.3
Matches 20; Conservative
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Best Local Similarity 83.3 Matches 20; Conservative
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ORGANISM: Unknown
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          US-09-907-719-43
                                                                Query Match
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Patent No. US/0020172997A1
GENERAL INFORMATION;
GENERAL INFORMATION;
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: OF INVENTION: Recombination Sites
FILE REPRESENCE: 0942.2850004
CURRENT APPLICATION NUMBER: 09407,900
CURRENT APPLICATION NUMBER: 09/177,387
PRIOR APPLICATION NUMBER: 09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFRENCE: 0942.2850004
CURRANT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 25
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OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
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Pred. No. 5.6;
                                                                              Score 21.2; DB 9;
Pred. No. 5.6;
3; Mismatches 1;
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Sequence 43. Application US/09907719
Publication No. US20020192819A1
GENERAL INFORMATION:
                                                                           Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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Best Local Similarity 83.3%;
Matches 20; Conservative
; OTHER INFORMATION: products US-09-855-797A-43
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; OTHER INFORMATION: products
US-09-907-900-43
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ORGANISM: Unknown
FEATURE:
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ORGANISM: Unknown
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Gaps

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Length 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 3, 2003, 17:22:25
Job time : 107.107 secs
                                                                                                                                                                                                                                                                                                                                                24 CAAGTTAGTATAAAAAGCTGAAC 1
                         ; ORGANISM: attR0
US-10-151-690-28
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                                                                                                                                                                                                                                                                                                                                 Cheo, David

Cheo, David

Bracch, Michael A.

APPLICANT: Bracch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Hartley, James L.

APPLICANT: Hartley, James L.

APPLICANT: Hartley, James L.

APPLICANT: Hartley, James L.

TITLE OF INVENTION: Recombinational Cloning

CURRENT FILING DATE: 2000-12-11

PRIOR PELICATION NUMBER: US 60/188,020

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patentin Version

IFFE.

TYPE: TITLE OF INVENTION CONTRIBUTION CONTRI
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Publication No. US20030124555A1
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: E1, XIAO
APPLICANT: BXRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOLETIE REPERENCE: 0942.5120001
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FEATURE:
JOTHER INFORMATION: Description of Unknown Organism: recombination US-10-300-992-43
                                                                                                                                                                                             Length 25,
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91.7%; Pred. No. 8.5;
tive 0; Mismatches
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PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 27
TYPE: DNA
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; ORGANISM: attRO
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December 3, 2003, 12:13:41; Search time 114.843 Seconds (without alignments) 564.131 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	7	24	100.0	24	22	AAF61395	Expression vertor
O	m	24	100.0		22	AAF61425	AttP* DNA fragment
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## ALIGNMENTS

AAF61394 standard; DNA; 24 BP.

AAF61394/c RESULT 1

Sequence-specific recombination, SSR, integrase, gene therapy; somatic; targeted integration; attP; attP\*; PCR primer; ss. Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect Expression vector pKEX-2-XR attP and attP\* PCR primer 03. 99DE-1041186 99DE-1041186 (first entry) WPI; 2001-246016/26. (DROE/) DROEGE P. DE19941186-A1. 30-AUG-1999; 30-AUG-1999; 01-MAR-2001. 05-JUN-2001 Synthetic. Droege P; AAF61394; PRANTANA

us-10-082-772-4.rng

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Gaps

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100.0%; Score 24; DB 22; Length 24; 100.0%; Pred. No. 0.28;

0.28;

0; Mismatches

Best Local Similarity 100. Matches 24, Conservative

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Query Match

24

CAACTTAGTATCAAAAAGCTGAAC 1 CAACTTAGTATCAAAAAGCTGAAC

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                                                                                                                                   This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sometic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
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       recombination between att sites
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                                                                                                                                                                 Sequence-specific recombination, SSR, integrase, gene therapy; somatic, targeted integration, attP*, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transfer to animal or plant cells. The method is simple and controllable and provides stable and targeted integration of selected DNA sequences.
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                                  AAF61425 standard; DNA; 27
                                                                                                (first entry)
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                                                                                                                                AttP* DNA fragment.
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RESULT 3
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Sequence 24 BP; 11 A; 5 C; 3 G; 5 T; 0 other;

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This invention describes a novel sequence-specific recombination (SSR) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA in a eukaryotic cell, comprising introducing two DNA sequences (1, 11) into a cell, using an integrase (int) to effect SSR. The invention also describes (1, a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant calls the method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                          Sequence-specific recombination, SSR; integrase; gene therapy; somatic; targeted integration; attP*; ds.
                                                                                                                                                                                                                                                                                                                                           Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
Lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 243 BP; 74 A; 34 C; 34 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phage-lambda recombination site atP01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 CAACTTAGTATCAAAAAGCTGAAC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAACTTAGTATCAAAAAGCTGAAC 24
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 14; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%;
Matches 24; Conservative (
                                                                                                                                                                                                99DE-1041186,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
AASO6175/c
ID AASO6175 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2000; 2000WO-US33546
                             E. coli attP* DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0169983
05-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage lambda;
                                                                                                                                                                                                                                                                                                                 WPI; 2001-246016/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage lambda
                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                       (DROE/) DROEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200142509-A1
                                                                                                                                    DE19941186-A1
                                                                                                                                                                                              30-AUG-1999;
                                                                                                                                                                                                                           30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1999;
                                                                                                                                                               01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS06175;
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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda att sequences are recognised by the recombination protein lambda of hybrid nucleic acids comprising mixing at least a first population of hybrid nucleic acids comprising mixing at least a first population of one target nucleic acid comprising one or more recombination sites with at least coursing some or all of the nucleic acids to recombine with all or some of hybrid nucleic acids. The method is useful for producing a population of the target nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins or peptides and they may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of
                                                                                                                                                                                                                                                     therapeutic
                                                                                                                                                                                                                                          Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                  Byrd DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 93.3%; Score 22.4; DB 22; Local Similarity 95.8%; Pred. No. 1.4; les 23; Conservative 0; Mismatches 1;
                                                                                                                                                              Temple GF, Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 6 A; 4 C; 5 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAACTTAGTATCAAAAAGCTGAAC 24
                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 24A; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two or more different nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 CAACTTAGTATAAAAAGCTGAAC
  09-MAR-2000; 2000US-0188020
                                     (CHEO/) CHEO D.
(BRAS/) BRASCH M A.
(TEMP) TEMPLE G F.
(HART/) HARTLEY J L.
(BYRD/) BYRD D R N.
                                         CHEO D.
BRASCH M A.
TEMPLE G F.
HARTLEY J L.
                                                                                                                                                              Brasch MA,
                                                                                                                                                                                                     WPI; 2001-356174/37
                                                                                                                                                                                                                                                                                                        e.g. Cre
                                                                                                                                                              Theo D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.

AAF61424 standard; DNA; 27

AAF61424/

RESULT 6

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Gaps . 0

Score 24; DB 22; Length 243; Pred. No. 0.33; Mismatches 0; Indels (

0; Mismatches

100.0%;

05-JUN-2001 (first entry)

AAF61424;

AttP DNA fragment.

ВЪ.

99DE-1041186 99DE-1041186

30-AUG-1999; 30-AUG-1999;

01-MAR-2001

DE19941186-A1 Unidentified

XX AX X B X B X B

WPI; 2001-246016/26

(DROE/) DROEGE

Droege P;

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DIA in a enkaryotic cell, comprising introducing two DNA sequences (1, 11) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                       Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                                                                                                                                                              sequence-specific recombination (SSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%; Score 22.4; DB 22;
95.8%; Pred. No. 1.4;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 BP; 6 A; 4 C; 5 G; 12 T; 0 other;
                                                                                                                       Disclosure; Fig 6B; 24pp; German
                                                                                                                                                                         This invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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CAACTTAGTATCAAAAAGCTGAAC 24 CAACTTAGTATAAAAAGCTGAAC 1 8 g

23; Conservative

Matches

.. 0

Gaps

. 0

Indels

ABZ58728 standard; DNA; 27 RESULT 7

BP

(first entry) 01-MAY-2003 ABZ58728;

Att site nucleotide sequence attP0

Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; att; ds.

Synthetic

WO200295055-A2

28-NOV-2002

21-MAY-2002; 2002WO-US15947.

21-MAY-2001; 2001US-291973P

(INVI-) INVITROGEN CORP

Byrd DRN Esposito D, Li X, Cheo D, WPI; 2003-129436/12 Brasch MA,

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid. Disclosure, Fig 13A; 273pp; English

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Gaps

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Indels

Score 22.4; DB 14; Pred. No. 1.6; 0; Mismatches 1;

93.3%;

23; Conservative

Matches

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Best

Local Similarity

Query Match

1 CAACTTAGTATCAAAAGCTGAAC 24 CAACTTAGTATAAAAAGCTGAAC 40

63

AAF61418 standard; DNA; 243 BP

AAF61418;

AAF61418/ ID AAF6: XX AC AAF6: XX

RESULT

Length 201;

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid and (d) causing some or all of the second population to recombine with some or all of the second target nucleic acid molecules to 

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form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. Sequences ABZ58727-762 represent att recombination site sequences used in the method of the
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chip for capturing a number of target polynucleotides. A group of these probes may be attached on cells which form part of a single chip. The oligonucleotides to be detected are labelled and are complementary to the set of capture probes used. The detection chip may be used to detect a number of different polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences given in AAQ50309-26 are probes which were used on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chip for capturing polynucleotide - has several different complementary probes fixed on cells at different sites on single
                                                                                                                               .;
0
                                                                                                   Length 27;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                    Probe; chip; cell; detection; label; capture probe; ss.
                                                                                              Score 22.4; DB 25;
Pred. No. 1.4;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 other;
                                                                    T; 0 other
                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 10pp; Japanese.
                                                                    Sequence 27 BP; 6 A; 4 C; 5 G; 12
                                                                                                                                                       1 CAACTTAGTATCAAAAAGCTGAAC
                                                                                                                                                                                  24 caacriagraraaaaaagcreaac
                                                                                                                                                                                                                                                        ВР.
                                                                                              Query Match
Best Local Similarity 95.8%;
Matches 23; Conservative
                                                                                                                                                                                                                                                     AAQ50319 standard; DNA; 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92JP-0042829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-330600/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HITA ) HITACHI LTD
                                                                                                                                                                                                                                                                                                                                           Detection probe 11
                                                                                                                                                                                                                                                                                                                                                                                                                             JP05236997-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          concurrently.
                                                                                                                                                                                                                                                                                                               27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1993
                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                   AAQ50319;
                                                                                                                                                                                                                                           AAQ50319/c
                                                                                                                                                                                                                           RESULT 8
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(first entry)

99DE-1041186.

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This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sometic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.
                                                            Sequence-specific recombination, SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                                                                                                                                                                                                                                                                                        Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 other;
                            Bacteriophage lambda attP DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACTTAGTATAAAAAGCTGAAC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAACTTAGTATCAAAAGCTGAAC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 13; 24pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 95.8%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC44676 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002WO-US17452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2003 (first entry)
                                                                                                        Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                             WPI; 2001-246016/26.
                                                                                                                                                                                                                                                                (DROE/) DROEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200297059-A2
                                                                                                                                        DE19941186-A1
                                                                                                                                                                                                   30-AUG-1999;
                                                                                                                                                                                                                                  30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus
05-JUN-2001
                                                                                                                                                                      01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC44676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                              Droege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
ACC44676/c
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Matches
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits sites thered integration in the presence of chromosome. Also described: (I) a platform artificial chromosome expression system (Accs) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an Accs. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection mammal) by introducing (II) by cell fusion, lipid-mediated transfection colly preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of Aces comprising readoms portions of a genome. ACC44612 exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                         Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                        Fleming E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                        Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other;
                                                                                                        Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.3%; Score 22.4; DB
95.8%; Pred. No. 1.7;
tive 0; Mismatches
                                                                  (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 CAACTTAGTATAAAAAGCTGAAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                                                                                    Lindenbaum M,
J;
                                                                                                                                                                                                                                                                             Example 2; Page 207; 272pp; English.
                 30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :636/c
ABT16636 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2002; 2002WO-US17451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001US-294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Conservative
                                                                                                      Perez C,
Shellard
                                                                                                                                                        WPI; 2003-140461/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WC200296923-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-2003
                                                                                                      Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
BXBXBXSXEEEEE
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Gaps ..

1; Indels

0; Mismatches

93.3%; Score 22.4; DB 22; Length 243; 95.8%; Pred, No. 1.7;

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The invention is a lover methods for targeting insertion of heterologous DNA into plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product the proteins, and proteins, and proteins, and proteins, and proteins, and proteins, inserts. AINA, structural proteins, and proteins, proteins, and proteins, vaccines, bloopharmaceutical proteins, vaccines, bloopharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heteroschogous nucleic acid is contained within a bacterial artificial heteroscome (BAC) or a yeast artificial chromosome (MAC). This producing plant artificial chromosomes of the invention.
                                                                                                                                                                                                                                                                has one or more repeat
                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to a novel method for producing plant artificial
                                                                                                                                                                                                                                                   plant cell, selecting artificial chromosome that has one or more re
regions with equivalent amounts of euchromatic and heterochromatic
nucleic acids
                                                                                                                                                                                                                                Producing artificial chromosome by introducing a nucleic acid into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 263-264; 269pp; English
                                             CHROMOS MOLECULAR SYSTEMS INC. AGRISOMA INC.
                                                                                                                                  Perkins E;
  04-JUN-2001; 2001US-296329P.
                                                                                                                          Perez C, Fabijanski SF,
                                                                                                                                                                                   WPI; 2003-140436/13
                                                     (CHRO-)
                                                                             (AGRI-)
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. Score 22.4; DB 25; Length 282; Pred. No. 1.7; 1; Indels 0; Mismatches 1 CAACTTAGTATCAAAAGCTGAAC 24 93.3%; 95.8%; 23; Conservative Local Similarity Query Match Matches à

ó:

Gaps

CAACTTAGTATAAAAAGCTGAAC 153 176 음

29-MAY-2001 AAF79770;

Bacteriophage lambda attachment P region. AAF79770 standard; DNA; 610 (first entry) 

Attachment P region; attP; recombination; marker gene removal; ds.

Bacteriophage lambda

WO200121780-A2

29-MAR-2001

15-SEP-2000; 2000WO-GB03543

99GB-0021937 17-SEP-1999;

(UYLE-) UNIV LEEDS

Meyer P,

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WPI; 2001-266072/27.
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Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene

Claim 8; Fig 3D; 25pp; English

The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibiotic resistance. The present sequence is the attP coding region. 

Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 other;

Gaps ó, 93.3%; Score 22.4; DB 22; Length 610; 95.8%; Pred. No. 1.8; i, 0; Mismatches Local Similarity 95.8 es 23; Conservative Query Match Matches

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300 CAACTTAGTATAAAAAGCTGAAC 277 1 CAACTTAGTATCAAAAAGCTGAAC 24 qq

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RESULT 13 AAZ30709 ID AAZ30

AAZ30709 standard; cDNA; 1763 BP

AAZ30709;

(first entry) 05-JAN-2000

Rat neuronal immediate early gene cDNA clone R280.

Immediate early gene; IEG; neuron; brain; function; growth factor; transcription factor; signal transduction; cytoskeletal protein; metabolic enzyme; learning; memory; synaptic transmission; tolerance; neuronal plasticity; ds.

Rattus sp.

W09940225-A1

12-AUG-1999

99WO-US02462. 05-FEB-1999;

98US-0074135. 09-FEB-1998; 12-FEB-1998;

(UVJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE (BADI ) BASF-LYNX BIOSCIENCE AG.

Scheek Kuner R, Hiemisch H, Goetz B, E; Lanahan A, Zhukovski Worley PF, Nikolich K, Worley 

WPI; 1999-590697/50.

treating conditions related stimulus -Novel genes and polypeptides, useful for a deficiency in nIEG responsiveness to a

Claim 1; Page 114-115; 134pp; English.

This sequence represents rat neuronal immediate early gene (IEG) cDNA clone R280. An IEG is a gene whose expression is rapidly increased immediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode a variety of proteins, including transcription factors, cytoskeleral proteins, growth factors and metabolic enzymes, as well as proteins involved in signal

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encode may provide important information about the function of neurons in, for example, learning, memory, synaptic transmission, tolerance and neuronal plasticity. Neuronal IEGs, neuronal IEG protein products, cells expressing neuronal IEGs and antibodies against neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG minimised. The deficiency may be a reduced or elevated level of expression of an IEG. The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IEGs and protein products are useful in identifying compounds that modulate the expression or activity of IEG nucleic acids or
The identification of neuronal IEGs and the proteins they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, respectively.
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Seguence 1763 BP; 478 A; 402 C; 452 G; 424 T; 7 other;

; 0 DB 20; Length 1763; Indels Score 22.4; DB; Pred. No. 1.9; 0; Mismatches 1 CAACTTAGTATCAAAAAGCTGAAC 24 93.3%; 95.8%; 23; Conservative Local Similarity Query Match Matches 8

Gaps

270 CAACTTAGTATAAAAAGCTGAAC 293 a

RESULT 14

ACC44716 standard; DNA; 4346 BP ACC44716;

(first entry) 29-MAY-2003

Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.

Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; gene; ds.

Bacteriophage lambda. Synthetic.

WO200297059-A2.

05-DEC-2002

30-MAY-2002; 2002WO-US17452.

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming Stewart S, Shellard J;

Ē

WPI; 2003-140461/13.

Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of interest

Example 3; Page 244-245; 272pp; English.

The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous mucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for ACC44716/C
LD ACC447716/C
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introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACse. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for the ACC44712 and ABP96650 to APB96657 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                          Score 22.4; DB 25; Length 4346; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Artificial plant chromosome related plasmid DNA SEQ ID No 26.
                                                                                                                                                                                                                                                                    Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Best Local Similarity
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Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids -Plant artificial chromosome; PAC; transgenic plant; vaccine; blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC; (CHRO-) CHROMOS MOLECULAR SYSTEMS INC щ Perkins 10-MAY-2002; 2002WO-US17451. 30-MAY-2001; 2001US-294687P. 04-JUN-2001; 2001US-296329P. Perez C, Fabijanski SF, AGRISOMA INC WPI; 2003-140436/13. WO200296923-A1. Unidentified. 05-DEC-2002. AGRI-) 

The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosome (PAC) is useful for producing a transgenic plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and biopharmacceutical proteins, vaccines, blood factors, antigens, hormones,

Example 19; Page 255-256; 269pp; English.

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cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents the DNA of a plasmid used in the method of the invention.

Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 other;

Gaps . 0 Query Match
93.3%; Score 22.4; DB 25; Length 4346;
Best Local Similarity 95.8%; Pred. No. 2;
Matches 23; Conservative 0; Mismatches 1; Indels 0;

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8 셤 Search completed: December 3, 2003, 12:23:36 Job time : 115.843 secs

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US-10-082-772-4/c ; Sequence 4, Application US/10082772
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Sequence 72, Appli
Sequence 57, Appl
Sequence 57, Appl
Sequence 13, Appl
Sequence 43, Appl
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Sequence 28, Appl
Sequence 42, Appl
                                                                                           December 3, 2003, 13:18:51; Search time 107.107 Seconds (without alignments) 744.732 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/US06 NEW_PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/US06 NEW_PUB.seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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4 US-10-161-403-72
2 US-09-244-805-57
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US-09-855-797A-43
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US-09-855-797A-42
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                             Seguence
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US-10-151-690-30
US-10-151-690-54
US-10-151-690-58
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APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITON OF N. M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOLI
FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US 10/151,690
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR PLING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PLING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
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Publication No. US20030119104A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                        BRASCH, MICHAEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.8<sup>3</sup>
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: attP0
US-10-151-690-26
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US-09-244-805-57/c
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APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Use of Multiple Recombinational Cloning
FILE REPERENCE: 0942.5010002
CURRENT APPLICATION NUMBER: US 60/169,983
FRICH FILING DATE: 2000-012-11
CURRENT PAPLICATION NUMBER: US 60/169,983
FRICH FILING DATE: US 60/169,983
FRICH FILING DATE: 1999-12-10
FRICH RELIGIATION NUMBER: US 60/188,020
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 27
            GENERAL INFORMATION:
APPLICANT: DROGE, PETER
APPLICANT: CHRIST, NICOLE
APPLICANT: CHRIST, NICOLE
APPLICANT: CHRIST, NICOLE
APPLICANT: CREACH, ELKE
TITLE OF INVENTION: SEQUENCE-SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REPREBACE: DEBE: 0.0819
CURRENT APPLICATION NUMBER: US/10/082,772
CURRENT APPLICATION NUMBER: PCT/DE 0.0/02947
PRIOR FILING DATE: 2000-08-29
PRIOR FILING DATE: 1999-08-30
NUMBER OS SEQ ID NOS: 20
SOFTWARE: PALENTIN UVER: 2.1
SEQ ID NO 4
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: Primer
US-10-082-772-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09732914
Patent No. US20020007051A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
Publication No. US20030027337A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
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Best Local Similarity
Matches 24; Conserva
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Best Local Similarity
Matches 23; Conserv
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; ORGANISM: attPO
US-09-732-914-2
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US-10-151-690-26
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Cloning Using Nucleic Acids Having
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          Indels
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APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: 00/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: pSV40-193AttpsensePur Plasmid
US-10-161-403-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Town Donna K.
TITLE OF INVENTION: Recombinational Cloning U
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850009
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 2001-05-16
          0; Mismatches
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95.8%; Pred. No. 4.
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                                                                                                                                                                                                                             Sequence 113, Application US/10161403
Publication No. US20030119104A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/09855797A Patent No. US20020094574A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,9
PRIOR FILING DATE: 1997-10-24
SUUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                             Perez, Carl
Lindenbaum, Michael
Greene, Amy
Leung, Josephine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
       23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative
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Best Local Similarity
Matches 23; Conserv
                                                          1 GTTCAGC
                                                                                                        293 GTTCAGC
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ORGANISM: Unknown
                                                                                                                                                                                                        1-403-113
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       Matches
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Publication No. US2030211984A1

GENERAL INFORMATION:

APPLICANT: Worley, Paul F.

APPLICANT: Lanahan, Anthony

TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: JHUISSO-3

CURRENT APPLICATION NUMBER: US/09/245,277

CURRENT APPLICATION NUMBER: 06/074,518

PRIOR FILING DATE: 1998-02-02

PRIOR FILING DATE: 1998-02-02

PRIOR FILING DATE: 1998-02-05

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 63

SOUTHARE FREEED FOR WINDOWS Version 4.0
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APPLICANT: Goetz, Bernard
APPLICANT: Goetz, Bernard
APPLICANT: Heimisch, Holger
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Dukovski, Eugene
ITLLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
ITLLE OF INVENTION: THEREFOR
FILE OF INVENTION: THEREFOR
FILE REPERENCE: 10496/004001
CURRENT APPLICATION NUMBER: US/09/244,805
CURRENT APPLICATION NUMBER: 60/074,518
EARLIER FILING DATE: 1998-02-12
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARE FILING DATE: 1998-02-06
SOFTWARE FILING DATE: 1998-02-06
SOFTWARE FILING DATE: Mindows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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, Application US/09244805
No. US20030203840A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57
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; OTHER INFORMATION: y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57
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Best Local Similarity
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ORGANISM: Eukaryote
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ORGANISM: Eukaryote
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LENGTH: 1763
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us-10-082-772-3.rnpb

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Sequence 43, Application US/09985448
| Sequence 43, Application US20030157716A1
| Publication No. US20030157716A1
| GENERAL INFORMATION:
| APPLICANT: Brasch, Michael A. |
| TITLE OF INVENTION: Recombination Sites FILE REPERENCE: 0942.2850004 |
| CURRENT APPLICATION NUMBER: US/09/177,387 |
| PRIOR PLING DATE: 1998-10-23 |
| PRIOR PRIING DATE: 1998-10-24 |
| NUMBER OF SEQ ID NOS: 60 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 43 |
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US-09-985-448-43
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                                                                     Length 25;
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                                                                     DB 10;
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                                                                 Query Match
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 20; Conservative 3; Mismatches
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Pred. No. 5.6;
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APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Fremble, Gary F.
APPLICANT: Fremble, Gary F.
TITLE OF INVENTION: Recombinational Cloning U TITLE OF INVENTION: Recombination Sites
CURRENT APPLICATION NUMBER: US/09/907,719
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GITCAGCITITIGATACTAAGTIG 24
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Sequence 43, Application US/10300892
Publication No. US20030175970A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 20; Conservative
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ORGANISM: Unknown
FEATURE:
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US-09-907-719-43
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Fublication No. US20020192819A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Donna K.
ITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.286004
CURRENT APPLICATION WUMBER: US/09/907, 719
CURRENT APPLICATION WUMBER: US/09/177,387
FRIOR APPLICATION WUMBER: US/09/177,387
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
TURNET 25
TYPE: DNA
THE OF MATCHING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/09907900
| Sequence 43, Application US/09907900
| Patent No. US20020172997al
| GENERAL INFORMATION:
| APPLICANT: Hartley, James L. |
| APPLICANT: Temple, Gary F. |
| TITLE OF INVENTION: Recombination Sites |
| TITLE OF INVENTION NUMBER: US0/09/907, 900 |
| CURRENT APPLICATION NUMBER: US0/177,387 |
| PRIOR FILING DATE: 1998-10-23 |
| NUMBER OF SEQ ID NOS: 60 |
| SOFTWARE: PatentIn Ver. 2.0 |
| LENGTH: 25 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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88.3%; Score 21.2; DB 10; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 20; Conservative 3; Mismatches 1; Indels (
                                                                                                             DB 9; Length 25;
                                                                                                                                                                               1; Indels
                                                                                                          Score 21,2; D. Pred. No. 5.6; 3; Mismatches
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                                                                                                                                                                                                                                                     1 GTTCAGCTTTTTGATACTAAGTTG 24
                                                                                                                                                                                                                                                                                                                           1 GTTCAGCTTTYTRACWAAGTTG 24
                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
       ; OTHER INFORMATION: products US-09-855-797A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
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US-09-907-900-43
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                                                                                          86.7%; Score 20.8; DB 14; Length 27; 91.7%; Pred. No. 8.5; cive 0; Mismatches 2; Indels
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Job time: 108:107 secs
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Best Local Similarity 91.7
Matches 22; Conservative
      , ORGANISM: attR0
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APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Byrd, Devon R.N.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning
TITLE OF INVENTION: Recombinational Cloning
TITLE OF INVENTION: Recombinational Cloning
TITLE OF INVENTION: UNMERR: US 60/169,983
CURRENT APPLICATION NUMBER: US 60/169,983
PRIOR PILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 2000-03-09
NUMBER OF SOC ID NOS: 140
SOFTWARE: Patentin version 3.0
LENGTH: 27
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Sequence 28, Application US/2030124555A1
Sequence 28, Application No. US20030124555A1
Sequence 28, Application No. US2003012455A1
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
FILE REFERENCE: 0942-5120001
CURRENT FILING DATE: 2002-05-21
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PILING DATE: 2001-05-21
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
; OTHER INFORMATION: products
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88.3%; Score 21.2; DB 12;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 20; Conservative 3; Mismatches 1;
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